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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                              SPTREMBL_17:*
1: sp_archea:*
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Gapop 10.0 , Gapext 0.5
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4225
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Copyright (c) 1993 - 2000 Compugen Ltd.
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sp_bacteria:*
sp_fungi:*
                                                                                                                     sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                     sp_organelle:*
sp_phage:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	80	7	6	ហ	4	ω	N	_	Result
113.5	114	121.5	145	161	350	471.5	490.5	514.5	697.5	1140	1413.5	1458.5	1473.5	1482	1853.5	1914	2945	4225	Score
2.7	2.7	2.9	3.4	3.8	8.3	11.2	11.6	12.2	16.5	27.0	33.5	34.5	34.9	35.1	43.9	45.3	69.7	100.0	Query Match L
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Q04049 saccharomyc	061391 caenorhabdi	P74506 synechocyst	Q42092 arabidopsis	Q9av63 oryza sativ	Q42099 arabidopsis	004607 arabidopsis	Q39466 cicer ariet	Q9fvm2 arabidopsis	Q9m442 cicer ariet	Q9lfz7 arabidopsis	Q9m4m7 persea amer	Q9scml arabidopsis	Q43408 brassica ol	Q40077 hordeum vul	Q9syj4 arabidopsis	Q9sbz0 phaseolus a	Q9fnd9 arabidopsis	. Q9zt62 cucumis sat	Description

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ALIGNMENTS

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Matches 544
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C Q9FND9;

Ol-MAR-2001 (TrEMBLrel. 16, Created)

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E RAFFINOSE SYNTHASE PROTEIN.

A Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryoph

Spermatophyta; Magnoliophyta; eudicotyledons; co
eurosids II; Brassicales; Brassicaceae; Arabidop

(NCBL_TaxID-3702;

[1]
                                               "Tabata S.;
"Structural analysis of Arabidopsis thaliana c
Sequence features of the regions of 1,044,062
Sequence features of the regions of 1,044,062
physically assigned P1 clones.";
DNA Res. 4:291-300(1997).
EMBL; AB006702; BAB11595.1;
SEQUENCE 783 AA; 86237 MW; 3C37D1D7871888A
                                                                                                                  SEQUENCE FROM N.A.
STRAIN-COLUMBIA;
MEDLINE-98069011; PubMed-9405937;
Kotani H., Nakamura Y., Sato S.,
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          Similarity
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                                                             Q9SBZ0 PRELIMINARY; PRT; 857 AA.
Q9SBZ0;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2001 (TrEMBLrel. 16, Last annotation update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
QALACTINOL-RAFFINOSE GALACTOSYLTRANSFERASE (EC 2.4.1.67).
Phaseolus angularis (Adzuki bean) (Vigna angularis).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Roside eurosids I; Fabales; Fabaceae; Papilionoideae; Vigna.
  SEQUENCE
                                        NCBI_TaxID=3914;
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EMBL; Y19024; CAB64363.1; -
Transferase; Glycosyltransferase.
SEQUENCE 857 AA; 94949 MW; 85248C4B81165679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peterbauer T., Mucha J., Mayer U., Popp M., Gloessl J., Richter A.; "Synthesis of stachyose in seeds of adzuki bean (Vigna angularis). Molecular cloning and functional expression of stachyose synthase from adzuki bean.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20117502; PubMed=10652123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VPET-ESYVVIIPIIEKSFRSALHPGSDDHVKICAESGSTQVRASSFGAIAYVHVAETPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLNDMSSPFAIDGSDFTVNGHSFLSDVPENIVASPSPYTSI---DKSPVSV-----
                                                                                        LYLYQAKKLILSKP-SQDLDIALDPFEFELITVSPVTKLIQTSLHFAPIGLVNMLNTSGA
                                                                                                                          KSDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHAGDDPF
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                          IQELEYIE - - KDVKVKVKGGGRFLAYSTQSPKKFQLNGSDAAFQWLPDGKLTLNLAW - IE
                                                                           VYLNQAEVLHLMTPVSEPLQLTIQPSTFELYNFVPVEKLGSSNIKFAPIGLTNMFNSGGT
                                                                                                                                                     KFTGVIGAFNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIEWHSGENPISIEGVKTFA
                                                                                                                                                                                                                                                                                                                                 IPCKLSPGLVGTMKDLAVDKIVEGSIGLVHPHQANDLYDSMHSYLAQTGVTGVKIDVIHS
                                                                                                                                                                                                                                                                                                                                               IQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVIHL 412
                                                                                                                                                                                                                                                                                                                                                                                   ESNESGGCCCKAAECGGMKDFTTDLRTEFKGLDDVYVWHALCGGWGGVRPGTTHL-DSKI 428
                                                                                                                                                                                                                                                                                                                                                                                                                                     NAPSFNPETIKELISKGIEAEHLGKQAAAISAGGSDLAEIELMIVKVREEIDDLFGGKGK
                                               IQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRACRIDGEDVGFKYDQDQMVVVQVPWPID 771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.3%; Score 1914; DB 10; 43.8%; Pred. No. 2.8e-141; tive 139; Mismatches 243;
                                                                                                                                                                                                                                                                                                                                                                                                 -GMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLPEARV 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
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C Q9SYJ4;
C Q9SYJ4;
C Q9SYJ4;
T 01-MAY-2000 (TrEMBLrel. 13, Created)
T 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
T 01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
E PUTATIVE RAFFINOSE SYNTHASE OR SEED IMBIBITION PROTEIN.
N T7811.23 OR AT4G01970.
S Arabidopsis thaliana (Mouse-ear cress).
C Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
C Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot
C Spermatophyta; Trach
C Spermatophyta; Brassicaceae; Arabidopsis.
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Best Local
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STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
Huang E.N., Nascimento L., de la Bastide M., Habermann K
Preston R.R., Splegel L.A., See L.H., Shah R., Matero A.
O'Shaughnessy A., Rodriguez M., Shekher M., Swaby I., Sc
Parnell L.D., Dedhia N., MCCombie W.R.;
"Arabidopsis thaliana BAC T/Bil from chromosome IV near
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AC007138; AAD22659.1; -.
EMBL; AL161493; CAB80690.1; -.
SEQUENCE 807 AA; 90122 MW; 963DCD5A827B338B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M. Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M., Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                     MAPSFKNGGSNVVSFDGLNDM--SSPFAI------DGSDFTVNGHSFLSDV
                                                                                                                                                                                                                                                                                          SIFREKVWWTTHWVGRNGGDLESETQIVILE--KSDSGRPYVFLLPIVEGPERTSIQPGD 150
                   HALCGYWGGLRPQVPGLPEARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMY
                                                                                                                                                                                                                                                                                                                                                                            PENIVASP-SPYTSIDKSPVSV------GCFVGFDASEPDSRHVVSIGKLKDIRFM 92
                                                                                                                                                                                                                                                                                                                                                                                                                MAPLHE-----SLSSINDVIESKPLFVPITKPILQPNSFNLSEGSLCAKDSTPILFDV
HALCGAWNGVRPETMMDLKAKVAPFELSPSLGATMADLAVDKVVEAGIGLVHPSKAHEFY
                                                                 NLVLGGEQMTARLTSFKECKKFRNYKEESLGSDDVSGSGMAAFTKDLRLRFKSLDDIYVW
                                                                                                                                IVDKFGWCTWDAFYLTVHPQGVIEGVRHLVDGGCPPGLVLIDDGWQSIGHDSDPITKEGM
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                                                                                                NQTVAGEQMPCRLLKFQENYKFRDYVNPKATGPRAGQKGMKAFIDELKGEFKTVEHVYVW
                                                                                                                                                                                                                                                                       SLFRFKMWWSTAWIGKSGSDLQAETQWVMLKIPEIDS---YVAIIPTIEGAFRASLTPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366;
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Pred. No. 1.4e-
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Schutz K.,
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Q40077;
01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-OCT-2000 (TREMBLREL. 1
SEED IMBIBITION PROTEIN.
                                                                                                                                                                                                                                                                                           Heck G.R., Dorsett C., Ho T.H.;
Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
EMBL, M77475; CAA32975 1;
Mendel; 116898; Horvu; 1149; 16898.
SEQUENCE 757 AA; 82133 MW; EA9E7B771AABBCCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooida
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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KHTQTFHHREKKTVPSFVDWFGWCTWDAFYTDVTADGVKQGLRSLAEGGAPPRFLIIDDG
              THLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVHPQGVIEGVRHLVDGGCPPGLVLIDDG
                                                    LPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHAGDDPFALVKEAMKIVR
                                                                                                            DIRFMSIFRFKVWWTTHWVGRNGGDLESETQIVILE------KSDSGRPYVFL
                                                                                                                                                                 KCYLNDKEAEFKWEEETGKLSFFVPWV--EESGGISHLSFTF 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACRIDGEDVGFKYDQDQ-MVVVQVPWPIDSSSGGISVIEYLF 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FVPVTELVSSGVRFAPLGLINMENCVGTVQDMKVTGD-NSIRVDVKGEGRFMAYSSSAPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSPVTKLIQTSLHFAPIGLVNMLNTSGAIQSVDYDDDLSSVEIGVKGCGEMRVFASKKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VHVSDIEW---DQNPEAAGSQVTYTGDYLVYKQQSEEILFMNSKSEAMKITLEPSAFDLLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEHCNDFMFLGTEAISLGRVGDDFWCTDPSGDPNGTFWLQGCHMVHCANDSLWMGNFIHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSMHSYLASVGVTGAKIDVFQTLESLAEEHGGRVELAKAYYDGLTESMIKNFNGTDVIAS
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                       35.1%; Score 1482; 39.4%; Pred. No. 1
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91, Last sequence update)
95, Last annotation update)
                                                                                                                                                                                                                           128;
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1.8e~107;
hes 266;
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Matches 297; Conserv
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Q43408;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-NOV-1996 (TrEMBLrel. 12, Last annotation update)
PUTATIVE IMBIBITION PROTEIN.
Brassica oleracea (Cauliflower).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID=3712;
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Fujikura Y., Karssen C.K.;
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ database
EMBL; X79330; CAR55893.1; -.
Mendel; 30784; Braol:1449;30784.
SEQUENCE 765 AA; 84084 MW; 73398603048E9B58 CRC64;
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NCBI_TaxID-3702;
EU Arabidopsis sequencing project;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL133248; CAB66109.1; -
SEQUENCE 773 AA; 85143 MW; 0852F9E67952C8D3 CRC64;
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Benes V., Rechmann S., Borkova D., Ansorge W.,
Mayer K.F.X., Quetier F., Salanoubat M.;
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"Isolation and characterization of cDNAs for mRNAs regulated vold storage of avocado (Persea americana Mill.) fruit.";

Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ133148; CAB77245.1;

EMBL; AJ133148; CAB77245.1;

CAB77245.1;

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                                                                                                                                                                                                                                                                                                                                      LLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QALEGSIARNFPDNGCIACMCHNTDSIY-SAKQTAVVRASDDFYPRDPAS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLGRVGDDFWCTDPSGDPNGTFWLQG
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                                                                                                                                                                      KLILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPIGLVNMLNTSGAIQSVD---
                                                                                                                                                                                                                                                             CRETRRNQCFSQYSKRVTSKTNPKDIE------WHSGENPISIEGVKTFALYLYQAK
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GFKYDQ-DQMVVVQVPWP
                                         DSNNAEPPLFDGKVASKLSSSLSNNQSPSATVVLRVRGCGRFGAYSSQRPLKCTVDLVET
                                                                                                                                EVVRLPKCASIPVTLEVLEYELXHICPV-KEITSNISFAPIGLLDMFNSGGAVEQFDVRM
                                                                                                                                                                                                                    CKITKKTRIHDAAPGTLSGSIRAHDVEFINQLAGQDW-NGE-----VIVFTYGSG
                                                                                                                                                                                                                                                                                                           LLKKLVLPDGSVLRARLPGRPTRDSLFVDPARDGVSLLKIWNMNKCLGVVGVFNCQGAGW
                                                                                                                                                                                                                                                                                                                                                                                                -HTIHVSSVANNSLFLGEFMQPDWDMFHSLHPAAEYHGAARAVGGCPIYVSDKPGHHNFE
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Pred. No. 4.4
                                                                                      -----VEIGVKGCGEMRVFASKKPRACRIDGEDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shinn P.P., Buehler E.E., Dunn P.P., Feng J.J., Kim C.C., Li Y.Y. Walker M.M., Altafi H.H., Araujo R.R., Conn L.L., Conway A.A.B., Gonzalez A.A., Hansen N.N.F., Huizar L.L., Kremenetskaia I.I., Lenz C.C., Li J.J., Liu S.S., Luros S.S., Rowley D.D., Schwartz Toriumi M.M., Vysotskaia V.V., Yu G.G., Davis R.R.W., Federspiel N.N.A., Theologis A.A., Ecker J.J.R., Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE FROM N.A.

Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C., Khan S., Brooks S., Buehler E., Chin C., Chiou J., Choi E., Conn L., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J., Conway A., Gonzales A., Liu K., Liu S., Mukharsky N., Nguyen M., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000
01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-2000)
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                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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AIDGSDFTVNGHSFLSDVPENIVASP-SPYTSIDKSPVSVGCFVGFDASEPDSRHVVSIG
                                                SVTDSDLVVLGHRVLHGVPENVLVTPASGNALID-----
                                                                                                                                                                                               AC002328;
NCE 1170
                                                                                                                               Similarity
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                                                                                                                  Conservative
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AA; 129057 MW;
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                                                                                                                  135;
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Last annotation updat
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                                                                                                                               Score 1140; DB 10;
Pred. No. 2.4e-80;
                                                                                                                  Mismatches
                                                                                                                                                                                               98B43A04E3F66D44 CRC64;
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                                                    -GAFIGVTSDQTGSHRVFSLG
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                                                                                                                     Indels
                                                                                                                                                Length 1170;
                    DSGRPYVFLLP
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Query Match
Best Local Similarity
                                                                                                                                                                      Q9M442 PRELIMINARY; PRT; 386 AA.
Q9M442;
Q1-Q27-2000 (TrEMBLrel. 15, Created)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-QCT-2000 (TrEMBLrel. 17, Last annotation update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE IMBIBITION PROTEIN (FRAGMENT)
Cicer arietinum (Chickpea) (Garbanzo)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidieurosids I; Fabales; Fabaceae; Papillionoideae; Cicer
                                                                      STRAIN-CV. CASTELLANA; TISSUE-ETIOLATED OSMOTIC STRESSED EPICOTYLS; Dopico B., Romo S., Labrador E.;
"A putative imbibition protein is expressed in chickpea epicotyls." Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ271668; CAB71135.1; -.
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                                                  SEQUENCE
                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                NCBI_TaxID=3827;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GGCPPGLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQMPCRLLKFQENYKFRD
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                                                   386 AA;
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                                                     42180 MW;
 16.5%;
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Pred.
                                                   357AF9FBC8D71650
  697.5; DB 1
No. 2.1e-46;
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                 Length
                                                                                                       epicotyls.";
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Best Local Similarity
Matches 118; Conserv
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01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
SEED IMBIBITION PROTEIN (FRAGMENT).
DIN10.
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NON_TER
NON_TER
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-1999) to the EMBL/GenBank/DDBJ EMBL; AF159378; AAG23721.1; -. Interpro; IPR000719; Euk_pkinase. PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thaliana.";
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                                                                                                                                                                                     221 DAFYLTVHPQGVIEGVRHLVDGGCPPGLVLIDDGWQSIGHDSDPITKEGMNQTV-AGEQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identification of novel dark-inducible genes
     336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEVYALPTRDCLFEDPLHNGETMLKI 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MRVFASKKPRACRIDGEDVGFKYDQDQ-MVVVQVPWP 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENPISIEGVKTFALYLYQAKKLILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FGVYSSQHPLQCAVDGIDTDFNYDSETGLTTFSIPVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGLMDMFNTGGAVEEVEIHKASDNKQELFDGEVVSELTTSLSPNRTKTATVALKVRGSGK 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGLVNMLNTSGAIQSVD------YDDDL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ET-----IVYAYRSGEVIRLPKGVSIPVTLKVLEFELFHFCPIQE-IAPSISFAA
YWGGLRPQVPGLPEARVIQ-PVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLH
                                                                                                                                            DAFYQEVTQEGVEAGLKSLAAGGTPPKFVIIDDGWQSVERDA-----TVEAGDEK
                                                     KESPIFRLTGIKENEKFK----
                                                                                      P----CRLLKFQENYKFRDYVNPKATGPRAGQKGMKAFIDELKGEFKTVEHVYVWHALCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                               283
283 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yoshikawa Y.,
                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                    283
31240 MW;
                                                                                                                                                                                                                                                              12.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68;
                                                                                                                                                                                                                                          ; Score 514.5; DB 10; pred. No. 2.9e-32; 52; Mismatches 104;
                                                     KKDDPNVGIKNIVKIAKEKHG----LKYVYVWHAITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                       33C43B84E8540301 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N., Basanti B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₹
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                                                                                                                                                                                                                                                                                                  DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      databases
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                                                                                                                                                                                                                                                       <u>3</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                        Matches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q39466
Q39466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases EMBL; X95875; CAA65125.1; -. Mendel; 7745; Cicar;1449;7745.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cicer arietinum (Chickpea) (Garbanzo).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Cicer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLEL. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEED INHIBITION PROTEIN (FRAGMENT).
                           529 RAISGGPIYVSDSVGKHNFDLLKKLVLPDGS 559
                                                          277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=3827;
                                                                                                                                                                          161
                                                                                                                                                                                                                                                                                                                                                             267
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                                                                                                                                                                                                                                                                                                                                                    w
                                                                                                                                                                                                                              SKNKNGQNDEQIPGLKHLVDGVK-KHHNVKDVYVWHALAGYWGGVKPAATGMEHYDTAL
                                                                              DDFWCTDPSGDPNGTFWLQGCHMVH----CANDSLWMGNFTHPDWDMFQSTHPCAAFHAAS
                                                                                                                                LLEMLCEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLGRVG 471
                                                                                                                                                                    ATSAVTRS--TWNQPDIVMDSLAVHGLRLVHPRGFTSTNE-THAYLASCGVDGVKVDVQT
                                                                                                                                                                                      VIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVIH 411
                                                                                                                                                                                                                                                                                                                 GLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQMPCRLLK-----FQENYK--FRDYVNPK 299
RAIGGCQFMSVISQATTILIFLRSLVLADGS 356
                                                         DDFYPHDPAS-----
                                                                                                              LLRPLVLDTVVESRLHAAIIMRLRLPLLVTLLNNGCIACMCHNTDGLY-SAKQTAIVRAS
                                                                                                                                                                                                                                                          ATGPRAGQK-----GMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLPE---AR 351
                                                                                                                                                                                                                                                                                      RFLIM-----TMVGNRLKVKQSKGSGCVVQEGAQLLLGDWIRDA
                                                                                                                                                                                                                                                                                                                                              QQAVKAVEKHMQTFHHREKKRVPSFLDWFGWCTWDAFYTDVTAEGVEEGLKSLSEGGTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WDMFQSTHPCAAFHAAS 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WDMFHSVHPAAEYHASA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TDALYCSKQAAVI-RASDDFYPRDPVS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NDFMFLGTEAISLGRVGDDFWCTDPSGDPNGTFWLQGCHMVHCAN---DSLWMGNFIHPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYLADAGVDGVKVDVQCVLETLGGGLGGRVELTRQFHQALDSSVAKNFPDNGCIACMSHN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YWGGVR---PGEEYGSVMKYPNMSKGVVENDPTWKTDVMTLQGLGLVSPKKVYKFYNELH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AHLEKVGIDGVKIDVIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        357
357
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357
39465 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                     11.6%;
                                                       --HTIHISSVAYNSLFLGEFMQPDWDMFHSLHPAAEYHAAA
                                                                                                                                                                                                                                                                                                                                                                                                        55;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 490.5; DB 10; Length Pred. No. 3.2e-30; 5; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E8CD30399E1BF3EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    357
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RESULT 004607 ID 600 OD TO 011 OD TO 011 OD TO 011 OD TO 011 OD TO 012 OD TO
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O04607 PRELIMINARY; PRT; 371 AA.
O04607;
O04607;
O1-JUL-1997 (TrEMBLrel. 04, Created)
O1-JUL-1997 (TrEMBLrel. 04, Last sequence update)
O1-WV-1999 (TrEMBLrel. 12, Last annotation update)
SIMILAR TO SEED IMBIBITION PROTEIN.
A_IGO2N01.5.
Arabidopsis thaliana (Mouse-ear cress).
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidieurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-1997) to the EMBL/GenBank/DDBJ EMBL; AF007269; AAB61043.1; -. Mendel; 16897; Arath; 1449; 16897. SEQUENCE 371 AA; 41564 MW; 9AEA7712D348344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-CV. COLUMBIA; Scheet P., Maggi L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-1997)
      365
                                                                                                                           318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CV.
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                                                                                                                                                                                                                                                                                                             442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 VGRNGGDLESETQIVILEKS------DSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 MGTNGKEIPCETQFLIVEANKGSGLGGGDESSSYVVFLPILEGDFRAVFQGNEANELEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13
                                                  LPDGSIL 561
LQDGSIL 371
                                                                                                                     YNTLFLGEFMQPDWDISSSSWRMCHLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTVEHVYVWHALCGYWGGLRPQVPGLPEARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLV 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VESGSSKVVDASFRSMLYLHAGDDPFALVKEAMKIVRTHLGTFRLLEEKTPPGIVDKFGW
                                                                                                                                                                                 -DSLWMGNFIHPDWDMFQST----HPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLV
                                                                                                                                                                                                                                                 FPANGKHRDLQYC---
                                                                                                                                                                                                                                                                                                    FKGNGVIASMEHCNDFMFLGTEAISLGRVGDDFWCTDPSGDPNGTFWLQGCHMVHCAN--
                                                                                                                                                                                                                                                                                                                                                                                                          PPEKAEEMYEGLHAHLEKVGIDGVKIDVIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSLKYYYVWHAITGYWGGVKPSVSGI--------MSNENCGC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NADSAA-NFANRLTHIKEKHKFQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NQTVAGEQMPCRLLKFQENYKFRDYVNPKATGPRAGQKGMKA-----FIDELKGEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTWDAFYRKVLRDCDLTKPAIILCSLK---AGVVTPKFVIIDDGWQSVGMDE---TSVEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTWDAFYLTV-----HPQGVIEGVRHLVDGGCPPGLVLIDDGWQSIGHDSDPITKEGM 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LESGK-----KLFMPDMLNWFGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COLUMBIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.2%;
26.9%;
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                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN-CV. NIPPONBARE;

Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Burr P.C.,

Hslao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,

Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,

Quackenbush J., White O., Salzberg S.L., Fraser C.M.;

"Oryza sativa chromosome 10 BAC OSJNBa0006L06 genomic sequence.";

Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AC022457; AAK27823.1; -.

SEQUENCE 204 AA; 21044 MW; 94605813D078387C CRC64;
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Desprez T., Amselem J., Chiapello H., Caboche M., Hofte H.;
Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; 25468; CAB01251.1;
Mendel; 16899; Arath;1449;16899.
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE STACHYOSE SYNTHASE.
Oryza sativa (Rice)
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nes 61; Conserv
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-----LLERRISFVPIGLANMLNVGGAVQGFQTVKKDDGGGGDVVAEVAVKGAKEAYSS 117
                                                                                                                     KATASTASPPTSWRHGSGGGNGDGVDCFTVYFVEAQKLQLLRRNESFELTLEPFTYEL-- 63
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ative 14; Mismatches 19;
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Pred. No. 9e-05;
3; Mismatches
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Search completed: November 30, 2001, 09:45:02 Job time: 281 sec

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Post-processing: Minimum Match 0%
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Copyright (c) 1993 - 2000 Comp
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ALIGNMENTS

hypothetical protein AT4901970 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (C;Species: Arabidopsis thaliana (mouse-ear cress) (C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 C;Accession: C85025 (R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Rature 402, 769-777, 1999 C;Genetics: A;Gene: AT4g01970 A;Map position: 4 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-807 <5°0> A;Cross-references: GB:NC_001268; NID:g7268581; PIDN:CAB80690.1; GSPDB:GN00140 A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A;Reference number: A85001; MUID:20083488 A;Accession: C85025Query Match 43.9%; Score 1853.5; DB 2; Best Local Similarity 44.5%; Pred. No. 8.6e-139; Mismatches 257; 1 MAPSFKNGGSNVVSFDGLNDM--SSPFAI------DGSDFTVNGHSFLSDV HALCGYWGGLRPQVPGLPEARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMY 390 NQTVAGEQMPCRLLKFQENYKFRDYVNPKATGPRAGQKGMKAFIDELKGEFKTVEHVYVW 330 IVDKFGWCTWDAFYLTVHPQGVIEGVRHLVDGGCPPGLVLIDDGWQSIGHDSDPITKEGM SIFRFKVWWTTHWVGRNGGDLESETQIVILE--KSDSGRPYVFLLPIVEGPFRTSIQPGD 150 PONTETPESSHSISTDAPLPILLRVQANAHKGGFLGFTKESPSDRLTNSLGRFEDREFL MAPLHE-----SLSSINDVIESKPLFVPITKPILQPNSFNLSEGSLCAKDSTPILFDV HALCGAWNGVRPETMMDLKAKVAPFELSPSLGATMADLAVDKVVEAGIGLVHPSKAHEFY IVDKFGWCTWDACYLTVDPATIWTGVKEFEDGGVCPKFVIIDDGWQSINFDGDELDKDAE 290 DB 2; Length 807; Indels 53; 170 92 53 14;

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                                                         WQQIGSENKDDP----GV-AVQEGAQFASRLTGIRENTKFQSEHNQEET-----PGLKR
                                                                                            WQSIGHDS--DPITKEGMNQTVAGEQMPCRLLKFQENYKFRDYVNPKATGPRAGQKGMKA 312
                                                                                                                                  KHTQTFHHREKKTVPSFVDWFGWCTWDAFYTDVTADGVKQGLRSLAEGGAPPRFLIIDDG
                                                                                                                                                        THLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVHPQGVIEGVRHLVDGGCPPGLVLIDDG
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probable imbibition protein - wild cabbage C; Species; Brassica oleracea (wild cabbage) C; Date: 13-Jan.195 #sequence_revision 13-Jan C; Accession: S45033
K; Fujikura, Y; Karssen, C.K.
submitted to the EMBL Data Library, May 1994
A; Description: Cauliflower cDNA encoding a pia; Reference number: S45033
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A;Cross-references: EMBL:X79330; NID:g488786; PID:g488787
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AFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLP--EARVIQPVLSPGLQMTMEDLA
                                           WQQIENKEKDSNCLVQE-----GAQFATRLVGIKENAKFQKN-DPKDT----QVSGLK
                                                                       WQSIGH---DSDPITKEGMNQTVAGEQMPCRLLKFQENYKFRDYVNPKATGPRAGQKGMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative 155;
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oleracea (wild cabbage)
#sequence_revision 13-Jan-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.9%; Score 1473.5; DB 2; 37.6%; Pred. No. 1.2e-108; tive 155; Mismatches 253;
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A;ACCessacu.
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-773 <BEN>
A;Cross-references: EMBL:AL133248
A;Cross-references: cultivar Columbia;
                                                                                                                                                                                                                                                                    A; Map position: 3
A; Introns: 64/2; :
A; Note: T8H10.120
                                                                                                                                                                                                                                                                                                                                                                                                                                                               imbibition protein homolog - Arabidopsis thaliana
N;Alternate names: protein T8H10.120
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Accession: T46188
R;Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; Mewes, H.W.; Lemcke, K
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                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: 223014
A; Accession: T46188
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                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 294; Conserv
   118
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VFLPLLEGQFRAVLQGNEKNEIEICFESGDKAVETSQGTHLVYVHAGTNPFEVIRQSVKA 177
                  FLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHAGDDPFALVKEAMKI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVGLVTLNLP 750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVIHLLEMLCEDYGGRVDLAKA 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NTVTDEKPELSSSSVVSENRSPTALISLGVRGCGRFGAYSSQRPLRCAVDGTETEFNYDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YYKAMTKSINKHEKGNGVIASMEHCNDEMELGTEAISLGRVGDDEWCTDPSGDPNGTEWL
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                                                                                          VSIGKLKDIRFMSIFRFKVWWTTHWVGRNGGDLESETQIVILEK-----SDSGRPYV 132
                                                                                                                         ITSNISVQNDNLVVQGKTILTKIPDNIILTP----VTGNGFVSGSFIGATFEQSKSLHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----DYDDDLSS------VEIGVKGCGEMRVFASKKPRACRIDGEDVGFKYDQ 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKKLILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPIGLVNMLNTSGAIQSV--
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                                                                                                                                                                                                                                                                                   146/1; 176/2; 192/3; 223/2; 259/2;
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence Database, January
                                                                                                                                                                                                      34.58;
                                                                                                                                                                                         157;
                                                                                                                                                                                     Score 1458.5; DB 2
Pred. No. 1.9e-107;
7; Mismatches 249;
                                                                                                                                                                                                                                                                                                                                    BAC clone T8H10
                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                   300/2; 484/3; 507/2; 552/2; 625/1;
                                                                                                                                                                                       Indels 103;
                                                                                                                                                                                                                    Length
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                                         746 RIDGEDVGFKYDQD-QMVVVQVP 767
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AVESTETDFTYDAEVGLVTLNLP
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                                                                                                                                                                                                                                                                                                                        AFNCQGGGGCRETRRNQCFSQYSKRVTSKTNPKDI-----EWHSGENPISIEGVKT
                                                                                                                                                                                                                                                                                                                                                                                           DKPGNHNFDLLRKLVLPDGSVLRAKLPGRPTRDCLFADPARDGISLLKIWNMNKFTGIVG
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                                                                                            AIESIDINHVTDKNPEFFDGEISSASPALSDNRSPTALVSVSVRGCGRFGAYSSQRPLKC
                                                                                                                                                AIQSVD------YDDDLSS------VEIGVKGCGEMRVFASKKPRAC
                                                                                                                                                                                               -IVYAYRSGEVVRLPKGASIPLTLKVLEYELFHISPL-KEITENISFAPIGLVDMFNSSG
                                                                                                                                                                                                                                                                                                 VFNCQGAGWCKETKKNQIHDTSPGTLTGSIRADDADLISQVAGEDW-SGDS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGWQQIENKEKDENCVVQE-----GAQFATRLVGIKENAKFQ-----KSDQKD
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R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; Wi Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, ansen, N.F.; Hughes, B.; Huizar, L. A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Ser, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A:Reference and analysis of Chromosome 1 of the plant Arabidopsis. A:Reference number: A86141; MUID:21016719 C;Genetics: A;Gene: F20N2.14 A;Map position: A; Molecule type: Dt A; Residues: 1-1170 A; Reference number: A86141; A; Accession: C96599 protein F20N2 14 [imported] - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: C96599 A; Cross-references: A; Status: preliminary <STO> GB: AE005173; NID: 98778496; PIDN: AAF79504.1; GSPDB: GN00141 iel, N.A.; Kaul, S.; White, '
Conway, A.R.; Creasy, T.H.; A.M.; Sun, Khaykin, Maiti, R

æ : Ξ :..

Marzia

E.; Kim

O.; Alor Dewar,

A; Gene:

sip

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A; Residues: 1-357 <CER>
A; Cross references: EMBL: X95875; NID: g1212811
A; Experimental source: germinating seed
C; Genetics:
                                                                                                       R;Cervantes, E.
submitted to the EMBL Data Library, February 1996
A;Reference number: Z16718
A;Accession: T09530
                                                                                                                                                                         probable seed inhibition protein - chickpea (fragment)
C;Species: Cicer arietinum (chickpea, garbanzo)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change
C;Accession: T09530
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                                                                    A; Molecule type: mRNA
                                                                                    A; Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLH 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KTAVIRASDDFWPRDPAS------HTIHIASVAYNTLFLGEFMQPDWDMFHSLHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AISLGRYGDDFWCTDPSGDPNGTFWLQGCHMYHCAN---DSLWMGNFIHPDWDMFQSTHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVKVDVQNILETLGAGHGGRVKLAKKYHQALEASISRNEPDNGIISCMSHNTDGLY-SAK 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVKIDVIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLP--EARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YVNPKATGPRAGQKGMKA------FIDELKGEFKTVEHVYVWHALCGYWGGLRPQVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GGCPPGLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQMPCRLLKFQENYKFRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSQLKTSLCPNFFRM-----PDMLNWFGWCTWDAFYTNVTAKDVKQGLESNCDLTKPAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RTHLGT-----FRLLEEKTPPGIVDKFGWCTWDAFYLTVHPQGVIEGVRHLVD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHAGDDPFALVKEAMKIV--- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLEDLRFMCVFRFKLWWMTQRMGTNGKEIPCETQFLIVEANQGSDLGGRDQSSSYVVFLP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLKDIRFMSIFRFKVWWTTHWVGRNGGDLESETQIVILEKS------DSGRPYVFLLP 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVTDSDLVVLGHRVLHGVPENVLVTPASGNALID-----GAFIGVTSDQTGSHRVFSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIDGSDFTVNGHSFLSDVPENIVASP-SPYTSIDKSPVSVGCFVGFDASEPDSRHVVSIG
                                                                                                                                                                                                                                                                                                                                                                                                                        NPISIEGVKTFALYLYQAKKLILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPI
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                                                                                          from
                                                                                                                                                                                                                                                                                                                                                                                         --TSLPVTLMPREYEVFTVVPVKEFSDGS-KFAPV
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                                                                                          GB/EMBL/DDBJ
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C; Accession: T01717
R; Scheet, P.; Magg1, L.
submitted to the EMBL Data Library, June 19
A; Description: The sequence of A. thaliana
A; Reference number: Z14407
A; Accession: T01717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein A_IG002N01.5 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 19-Feb_1999 #sequence_revision 19-Feb-1999 #text
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A; Introns: 5/2; 25/3; 103/3; 126/1; 174/2;
A; Note: A_IG002N01.5
                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AF007269; NID:g2191126; PID:g2191156
A;Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-371 <SCH>
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Best Local Similarity
Matches 127; Conserv
                                                                                                                                                                                                                                 Query Match 11.2%; Score 471.5; DB 2; Best Local Similarity 26.9%; Pred. No. 1.5e-29; Matches 131; Conservative 71; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                             Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 KEAMKIVRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVHPQGVIEGVRHLVDGGCPP 246
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                                                                                                                                                                                             106 VGRNGGDLESETQIVILEKS-----DSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326
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  114
                                    218 CTWDAFYLTV-----HPQGVIEGVRHLVDGGCPPGLVLIDDGWQSIGHDSDPITKEGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 RFLIM-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQAVKAVEKHMQTFHHREKKRVPSFLDWFGWCTWDAFYTDVTAEGVEEGLKSLSEGGTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDFWCTDPSGDPNGTFWLQGCHMVH----CANDSLWMGNFIHPDWDMFQSTHPCAAFHAAS 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLEMLCEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLGRVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATSAVTRS--TWNQPDIVMDSLAVHGLRLVHPRGFTSTNE-THAYLASCGVDGVKVDVQT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQMPCRLLK-----FQENYK--FRDYVNPK
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  CTWDAFYRKVLRDCDLTKPAIILCSLK---AGVVTPKFVIIDDGWQSVGMDE---TSVEF
                                                                                                              VESGSSKVVDASFRSMLYLHAGDDPFALVKEAMKIVRTHLGTFRLLEEKTPPGIVDKFGW
                                                                                                                                                       MGTNGKEIPCETQFLIVEANKGSGLGGGDESSSYVVFLPILEGDFRAVFQGNEANELEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAIGGCQFMSVISQATTILIFLRSLVLADGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAISGGPIYVSDSVGKHNFDLLKKLVLPDGS 559
                                                                              LESGK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------TMVGNRLKVKQSKGSGCVVQEGAQLLLGDWIRDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.6%; Score 490.5; DB 2; 32.5%; Pred. No. 4.4e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55;
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                                                                                                                                                                                                                                                                                                                                                         240/1;
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                                                                                                                                                                                                                                                                                                                                                           284/1; 295/1;
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                                                                                                                                                                                                                                                                                                                                                           333/2;
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CiSpecies: Synechocystis sp.

A; Variety: PCC 6803

C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

C; Accession: S76481

R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, DNA Res. 3, 109-136, 1996
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A;Residues: 1-538 <KAN>
A;Cross-references: EMBL:D90915; GB:AB001339;
A;Note: the nucleotide sequence was submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: S74322; MUID:97061201
A;Accession: S76481
A;Status: preliminary
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Best Local S
Matches 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
                                                                                                                                                                                                                                               SRHV--VSIGKLKDI-----RFMSIFRFKVWWTTHWVGRNGGDLESETQIVILEKSDSGR
                                                                                                                                                                                                                                                                                                                       MSSPFAIDGSDFTVNGHSFLSDVPENIVASPSPYTSIDKSPVSVGCFVGFDASEPD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YNTLFLGEFMQPDWDISSSWRMCHLC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPEKAEEMYEGLHAHLEKVGIDGVKIDVIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NQTVAGEQMPCRLLKFQENYKFRDYVNPKATGPRAGQKGMKA-----FIDELKGEF
              D-YVNPKATGPRAGQKGMKAFIDEL-----KGEFKTVEHVYVWHALCGY-----
                                                              VDGGCPPG-LVLIDDG----WQSIGHDSDPITKEGMNQTVAGEQMP-CRLLKFQENYKFR
                                                                                                       LYQATDRIFTWLGKQEIPSNPVPPNLKPLALAEPGPQKWTTQNLTIPRPNGQPVNVFVYL
                                                                                                                                  VKEAMKIVRTHLGTFRLLEEKTPPGI----VDKFGWCTWDAFYLTV-HPQG-VIEGVRHL
                                                                                                                                                                  PF-----LEGAIVTAAQNPDGFKIIDVINAYGGSDLVLNLD-TFKNTI-----DQADT
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                                         PQGNSSPAPLVVIAPGLNSNFQAFTYIADHLASYGF--TIAGIDFPESDAARMQDSLQGL
                                                                                                                                                                                                 PYVFLLPIVEGPFRTSIQ-PGDDDFVDVCVESGSSKVV---DASFRSMLYLHAGDDPFAL
                                                                                                                                                                                                                               TQHLKPEELEKLRGLLNHSFKFNSVEAFRFFNTTF-----GKETAQQLSYIIAAPTDQSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -DSLWMGNFIHPDWDMFQST----HPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NADSAA-NFANRLTHIKEKHKFQ------KDGKEGHRVDDPALSLGHVITDIKSN-
                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                    2.98;
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                                                                                                                                                                                                                                                                                            -ETITFSIMPLGQFDISVKSLTDFAETGTIDPDFKFY
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Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                       Mismatches
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<u>::</u>
                                                                                                                                                                                                                                                                                                                                                                                                                               NID:g1653604; PIDN:BAA18610.1; PID:d10193. to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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                                                                                                                                                                                                                                                                                                                                                       185;
                                                                                                                                                                                                                                                                                                                                                                                    Length 538;
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Yamada, M.; Yasuda
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              436
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A:Map position: 3
A:Introns: 26/1
C:Superfamily: unassigned WD repeat proteins; WD repeat homology
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-902 <HIL>
A;Residues: 1-902 <HIL>
A;Cross-references: EMBL:AL031324; PIDN:CAA20445.1; GSPDB:GN00068; SPDB:SPCC1672.07
A;Experimental source: strain 972h-; cosmid c1672
A;Experimental source: strain 972h-; cosmid c1672
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A;Reference number: Z21967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          beta transducin - fission yeast (Schizosaccharomyces C; Species: Schizosaccharomyces pombe C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A; Accession: T41051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257 SIGHDSDPITKEGMNQTVAGEQMPCRLLKFQENYKFRDYVNPKATGPRAGQKGMKAFID- 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLQMTMEDLAVDKIVLHKVGLVPPEKAEEMY-----EGLHAHLEKVGIDGV-KIDVIHLL
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QHVLPTSDGTSVRSVCVSCCGNFGLIGSSKGVVDVYNMQSG-----IKRKSFGQSSLSG
                                                                                                                                QGSVISKAKKLNVRPEELKLPEITALSSSNTREKYWDNVLTAHKNDSSARTWNWKSKTLG
                                                                                                                                                                                                                                                         RSRNGHYEPPSFVKFYGKSVHFLISAATDRSLRAVS---LY-QDS-----QSTELS
                                                                                                                                                                                                                                                                                                                         ----GNFIHPDWDMF--QSTH--PCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLP
                                                                                                                                                                                                                                                                                                                                                                                         DLSFWDLSKRRIQNVTYNAHFGSLPKIQFLNGQPILVTAGPDNSLKEWIFDSMDGAPRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                      D-DFWCTDPSGDPNGTF-------WLQGCHMVHCA--NDSL--WM------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVLAVGTISGRI----VIFNLKNGSILMEFKQDGQVLSCSFRTD----GTPILASSNPIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NTNADITSLLHPSTYLNKILLGFSDGALQIWNLRVSKRVHEFQEFFG-DGITSLTQAPVL
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39; Conservative
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Pred. No. 1.1
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                                                                                                                                                                                      TRDCLFEDPL -- HNGETMLKIWNLNKFT--
                                                         -GVIGAFNCQGGGWCRETRRNQCFSQYS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
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RES S69	Db S	Db Oy	Q	Qu Be Ma Qy Db	TAESI PTO CONTRACTOR CONTRACTOR CONTRACTOR AND	2
SSULT 11	64 LGCKSFKWYLDNIYPELFVPGESVAKGEMRNAGGKNRQCIDYKPSGGKTVGMYQCH 96 HCANDSLWM 504 :	:: :: :: :: :: :: :: :: :: ::	279 MPCRLLKQENYKPKDYNNKAGGP	2.7%; Score 114; DB 2; Length 623; st Local Similarity 21.7%; Pred. No. 0.84; tches 80; Conservative 55; Mismatches 122; Indels 112; Ga 220 WDAFYLTVHPQGVIEGV-RHLVDGGCPPGLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQ 111	RESULT 10 T42245 probable polypeptide N-acetylgalactosaminyltransferase (EC 2.4.1.41) - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000 C; Accession: T42245 R; Hagen, F.K.; Nehrke, K. J. Biol. Chem. 273, 8268-8277, 1998 A;Title: CDNA cloning and expression of a family of UDP-N-acetyl-Dgalactosamine:Polypept A; Reference number: Z22126; MUID:98192620 A; Accession: T42245 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Residues: 1-623 < CHAG> A; Cross-references: EMBL:AF031835; NID:g3047190; PIDN:AACl3671.1; PID:g3047191 C; Genetics: A; Genetic	623 KRVTSKTNPKDIEWHSGENPISIEGVKTFALYLYQAKKLILSKPS 667

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submitted to the EMBL Data Library, August 1995
A; Description: The sequence of S. cerevisiae lambda 3641 and A; Reference number: S69555
A; Accession: S69702
A; Accession: S69702
A; Molecule type: DNA
A; Residues: 1-632 <DIE>
A; Cross = references: EMBL:U33007; NID:g927685; PIDN:AAB64856.1
C; Genetics: The Company of t
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A;Cross-references:
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                                                              FALYLYQAKKLIL--SKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPIGL 702
                                                                                                                                      IVDCISWLEVFCAELTSRIQDLEQEYNKIVIPRTYSISLKTKSYEVYRKSGPVAYKGIN-
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      -FQSHELLKVGIKFVTDLDI-----KGKNKSYYPLTKLSMTITNFDIIDL
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21.2%; Pred. No. 0.94;
1tive 55; Mismatches 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --LQGCHMVHCANDSLWMGNFIHPDW-----DMFQSTHPCAAFH 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -DGSILR 562
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RESULT 164118

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1,4-alpha-glucan branching enzyme (EC 2.4.1.18) - Haemophilus influenzae (strain C;Species: Haemophilus influenzae C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: I64118 A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae FA;Reference number: A64000; MUID:95350630
A;Accession: I64118 R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995 influenzae Rd Vente

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RESULT
T19997
                                                                                                                                   hypothetical protein C47D12.1 - Caenorhabditis elegans (;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te: C;Accession: T19997 R;Gajadsty, S.
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                     submitted to the EMBL Data Library, A;Reference number: Z19209 A;Accession: T19997 A;Status: preliminary; translated f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----SENFVLPLS---HDEVVHGKYSLLGKMPGDTWQKFANLRAYYGYMWGYPGK
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Pred. No. 5.
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                           GB/EMBL/DDBJ
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A; Residues: 1-3944 <WIL>
A; Cross-references: EMBL:Z69902; PIDN:CAA93765.1; GSPDB:GN00020; CESP:C47D12.1
A; Experimental source: clone C47D12
C; Genetics:
A; Gene: CESP:C47D12.1
A; Map position: 2
A; Introns: 46/3; 308/3; 408/2; 449/3; 820/3; 946/3; 1069/1; 1634/3; 1737/2; 200
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                             GLYNMLNTSGAIQSVD
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NMTNMMVSQLDIHAVD
                                                             LVYFQQNYNLDFLEIRNKRKMIVTKGCMGVEKSQIMFEKELSQVFTEPAGMQDEFDFV-T
                                                                                              ALYLYQ-----AKKLILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPI 700
                                                                                                                                RHLRHAICLKDQMFKDFSEQMDATFNEMQYSEDVTMMT----LRWR------KQLEED
                                                                                                                                                             EDYTDEQMSMDVSDEDCFADDPPF--DRILKICLKYRPTDIRVFHRVLKELDEMNETWVE
                                                                                                                                                                                                                       SEY-----YALPTRDCLFEDPLHNGETMLKI-----WNLNKFTGVIGAFNCQGGGW--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----LHKVGLVPPEKAEEMYEG-----LHAHLEKVGIDGVKIDVIHLLE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NKLAG-LTAIPMMDAQDKVCTYGKTLRDMANSAADERVKNELLCEALEV-LEDVRIDDLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLPEARVIQPVLSPGLQMTMEDLAVDKIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHAGDDPFALVKEAMKIVRTHLGT
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RESULT 14 HMIVF7

hemagglutinin precursor - influenza A virus (strain A/ruddy turnstone/NJ/47/85 [H4N6] N;Contains: hemagglutinin HA1; hemagglutinin HA2 C;Species: influenza A virus C;Species: influenza A virus C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 18-Sep-1998 C;Accession: G34214

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R;Donis, R.O.; Bean, W.J.; Kawaoka, Y.; Webster, R.G.

Virology 169, 408-417, 1989

A;Title: Distinct lineages of influenza virus H4 hemagglutinin genes in different region A;Reference number: A34214; MUID:89204912

A;Recession: G34214

A;Rocession: G34214

A;R
extracellular solute-binding protein -
N;Alternate names: hypothetical protein
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision
C;Accession: S74819
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 LANNGKF-EFIAEEFQWNTVKQNGKSGACKRANVNDFFR-RLNWLTKSDGNAYPLQNLTK 181
                                                                                                                                                                                                                                                                                                                       487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YLTVHPQGVIEGVRHLVDGGCPPGLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQMPCRL
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                                                                                                                                                                                                                                                                                                                       CDNNCI---ESIRNGTYDHDIYRDEAI---NNRFQIQGVKLTQGYKDIILWI 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                DTKIDLWSYNAELLVALENQH--TIDVTDSEMNKLFERVRRQLRENAEDKGNGCFEIFHQ
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; Pred. No. 5.9;
61; Mismatches
                                                                                                                              protein
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n slr1740
                                      25-Apr-1997
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R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Y DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacter
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:D90909; GB:AB001339; A;Note: the nucleotide sequence was submitted
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                                                                                                                                                                                                                                                                                                                                                                                         A; Start codon:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-582 <KAN>
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A; Status: nucleic a
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                                                                  106 VGRNGGDLESETQIVILEKSDSGRPYVF1LPIVEGPFR-TSIQPGD--
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                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                      52 SPYTSI-----DKSPVSVGCFVGFDASEPDSRHVVSIGKLKDIRFMSIFRFKVWWTTHW 105
                                                                                                                                                                                              97 PSVENGG----VAADGLSVTWKLKPDVLWSDGQPFSAEDVAFT----YKFLSD-PKTGATST 149
                                                                                                                                                                                                                                    3 PSFKNGGSNVVSFDGLN-----
  -DDFVDVCVESGSSKVVDASFRSMLYLHAGDDPFAL 185
                                        VGSEGMILPQHIYKDFVGEKARQAP-ANLLPIGTGPYRVTSFKPGDVVLYEVNPHYRDRK 240
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                                                                                                                                                                                                                                                                                             2.4%;
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Pred. No. 6.2;
20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y.; Miyajima,
Yamada, M.; Ya
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search completed: November 30, 2001, 09:41:50
Job time: 89 sec

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NIGFQQVEIKGGG----DATSAARAVLQTGDADFAL



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Result
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Compugen Ltd
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31.673 Million cell updates/sec
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Broad bean raffino Amino acid sequenc Japanese artichoke Amino acid sequenc Soybean protein: Soybean raffinose
                                                                                                                                      Cucumber raffinose
Cucumber raffinose
Cucumber raffinose
Cucumber raffinose
                                                                                                                                                                                                                                          Description
                                                                                                                          Soybean raffinose
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ALIGNMENTS

Fibroblast growth	AAR65931	15	135	33.1	60	45
Rat fibroblast gro	AAR65933	15	134	33.1	60	44
Human basic fibrob	AAP81932	9	134	33.1	60	43
Human basic fibrob	AAY17995	20	132	33.1	60	42
rhbFGF mutein CS23	AAP90564	10	129	33.1	60	41
rhbFGF mutein C129	AAP90562	10	129	33.1	60	40
asic fi	AAP81940	9	129	33.1	60	39
rhbFGF mutein C123	AAP90561	10	123	33.1	60	38
rhbFGF mutein C118	AAP90560	10	118	33.1	60	37
basic fi	AAB60696	22	114	33.1	60	36
'n	AAP90559	10	114	33.1	60	35
mutein	AAP90558	10	105	33.1	60	34
rhbFGF mutein CS10	AAP90557	10	101	33.1	60	33
H	AAP81933	9	86	33.1	60	32
unogenic pe	AAB18551	21	45	33.1	60	31
FGF antagonist bFG	AAR43278	14	45	33.1	60	30
	AAP71559	8	45	33.1	60	29
Immunogenic peptid	AAB18542	21	44	33.1	60	28
FGF residues 27-69	AAR24342	13	43	33.1	60	27
antagonist	AAR43286	14	40	33.1	60	26
FGF antagonist (Al	AAR43287	14	40	•	62	25
Basic fibroblast g	AAR03961	11	150	•	89	24
Soybean raffinose	AAY17419	20	10	39.2	71	23
	AAY70975	21	756	٠	97	22
t raffinos	AAY70981	21	841	•	98	21
Rice raffinose syn	AAY70976	21	770		102	20
ean raffino	AAY17418	20	750	58.6	106	19
affinose s	AAY70977	21	763		107	18
Wheat raffinose sy	AAY70980	21	751	59.7	108	17
Sugarbeet raffinos	AAY32073	20	783	67.4	122	16
Mustard raffinose	AAY32074	20	777	•	144	15
Rapeseed raffinose	AAY32075	20	572	79.6	144	14
Soybean raffinose	AAB49400	22	781	80.7	146	13
Amino acid sequenc	AAY30143	20	781	80.7	146	12

X PX PX SX X X PX PX A X I I RESULT AAW53567 Cucumis sativus Cucumber; raffinose synthase; sucrose; galactinol Cucumber raffinose synthase 06-JUL-1998 (first entry) AAW53567 standard; peptide; 30 JP10084973-A. AAW53567; _ residues 215 to 244. ₽

CCCXXX 07-APR-1998. WPI; 1998-264858/24. (AJIN) AJINOMOTO KK. 26-JUL-1996; 26-APR-1996; 28-APR-1997; 96JP-0198079. 96JP-0107682. 97JP-0111124

Claim 2; Page 16; 26pp; Japanese. Raffinose synthase gene - useful for transformed plant preparation of raffinose

The present sequence is a cucumber raffinose synthase fragment. Raffinose synthase forms raffinose from sucrose and galactinol, has

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RESULT
AAX17422
ID AAX1
XX AAX1
AC AAX1
XX Cuc
XX Cuc
XX Raf
XX PP
XX JP
RESULT
AAW53570
ID AAW5
XX
AC AAW5
XX
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Matches 30; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a raffinose synthase, having an activity of forming raffinose from sucrose and galactinol. The raffinose synthase gene can be used for expression in a plant for the production of raffinose. The raffinose synthase can give raffinose from sucrose and galactinol efficiently. The present sequence represents a raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                          AAW53570;
                                                                           AAW53570 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AJIN ) AJINOMOTO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cucumber raffinose synthase peptide SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthase peptide from cucumber.
                                                                                                                                                                                                                                                                                                                Local Similarity
tes 30; Conserv
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                                                                                                                                                                                                                                                                                                             100.0%; ilarity 100.0%; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
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                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sucrose; galactinol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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                                                                                784
                                                                                                                                                                                                                                                                                                                  0,
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Pred. No. 1.8e-19;
                                                                                                                                                                                                                                                                                                                                           Score 181; DB 20;
Pred. No. 1.8e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
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                                                                                B
                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                   Length 30;
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N-PSDB; AAX61238

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RESULT
AAY17417
ID AAY1
XX AAY1
XX CAY1
DT 29-J
XX CUCU
XX RAff
XX PAff
XX PAff
XX PAff
XX PAff
XX AAF1
XX JP11
XX JP1
XX JP11
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Best Local :
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26-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is cucumber raffinose synthase, which forms raffinose from sucrose and galactinol, has an optimum pH of 6 to 8 and working temperature of 35 to 40 degrees C, has a molecular weight of 75 to 95 kDa by gel filtration or 90 to 100 kDa by PAGE and SDS-PAGE under reductive conditions and is inhibited by iodoacetamide, N-ethylmaleimide and myoinositol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cucumber raffinose synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cucumis sativus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Pages 17-20; 26pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Raffinose synthase gene - useful for preparation of raffinose transformed plant % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-APR-1998
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                                                                                                                                                                                                                                                                                                                                              Cucumis sativus.
                                                                                                                                                                                                                                                                                                                                                                                           Raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Cucumber raffinose synthase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY17417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY17417 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                  WPI; 1999-340516/29
                                                                                             (AJIN ) AJINOMOTO KK
                                                                                                                                               24-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              784 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96JP-0198079
96JP-0107682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 181; DB 19; 100.0%; Pred. No. 8.2e-18; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        784 AA.
                                                                                                                                                                                                                                                                                                                                                                                           galactinol.
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RESULT
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Query Match
Best Local Similarity
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                             The present sequence is a raffinose synthase from clone sfl1.pk125.d4 isolated from a soybean immature flower cDNA library sfl1. Raffinose synthase is involved in the biosynthesis of raffinose and higher homologues in the raffinose saccharide family from sucrose. The present sequence is useful for reducing the raffinose saccharide content of soybean seeds which improves the nutritional quality of the soy protein products derived from them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a raffinose synthase, having an activity of forming raffinose from sucrose and galactinol. The raffinose synthase gene can be used for expression in a plant for the production of raffinose. The raffinose synthase can give raffinose from sucrose and galactinol efficiently. The present sequence represents raffinose
                                                                                                                                                                                           Claim 2; Page 47-49; 58pp;
                                                                                                                                                                                                                     Nucleic acids and encoded proteins involved in the biosynthesis of raffinose, useful for producing soybean seeds with a reduced raffinose content and therefore improved nutritional quality -
                                                                                                                                                                                                                                                                             WPI; 2000-350754/30.
N-PSDB; AAD00335.
                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soybean; raffinose synthase; raffinose saccharide; clone sfll.pk125.d4; nutritional; soy protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soybean raffinose synthase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New raffinose synthase gene - for production of raffinose from sucrose and galactinol \label{eq:sucrose}
                                                      Sequence
                                                                                                                                                                                                                                                                                                                       Allen
                                                                                                                                                                                                                                                                                                                                               (DUPO ) DU
                                                                                                                                                                                                                                                                                                                                                                                                        22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                     SM,
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                                                                                                                                                                                                                                                                                                                                                 PONT DE NEMOURS & CO E
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                                                        758 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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 87.3%;
86.7%;
                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from clone sfll.pkl25.d4
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 Score 158; DB 21; Pred. No. 1.7e-14;
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Pred. No. 8.2e-18;
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            Length 758;
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26-OCT-1999 AAY30142;

(first entry)

AAY30142 standard;

Protein;

799

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RESULT
AAY30142
ID AAY3
XX
AC AAY3
AC AAY3
XX
DT 26-0
XX
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Best Local S
Matches 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the broad bean raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides in the host organism or cell is changed. Raffinose oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 26-29; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oeda K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Raffinose synthetase; metabolism modification; food additive; gastrointestinal flora; broad bean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Broad bean raffinose synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW57886;
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DB; AAV40800.
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                                                                                                                                                                                                                                                                                                                                                             24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        799
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96JP-0338673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97EP-0122417.
                                                                                                                                                                                                                                                                                                                                                                                  81.8%;
                                                                                                                                                                                                                                                                                                                                                        ; Score 148; DB
; Pred. No. 5.2e
2; Mismatches
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                                                                                                                                                                                                                                                          267
                                                                                                                                                                                                                                                                                                          30
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                                                                                                                                                                                                                                                                                                                                                                                  DB 19;
.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                          19;
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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AAW5788
AAW5788
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Page 19-21; 40pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-NOV-1997;
18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP11215984-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a raffinose synthase protein. The sequence is isolated from plant material of broad beans. The protein forms raffinose by complexing alpha(1 to 6)- D-galactosyl hydroxyl group of the 6C of D-glucose residue in sucrose molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAZ10001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New raffinose synthase gene - is prepared from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SUMO ) SUMITOMO CHEM CO LTD
New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with
                                                                                                                                                                                                                                                                                     18-DEC-1997;
                                                                                                                                                                                                                                                                                                                                 24-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                            Stachys sieboldii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gastrointestinal flora; Japanese artichoke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Japanese artichoke raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW57888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                       N-PSDB; AAV40802.
                                                                                          WPI; 1998-324670/29.
                                                                                                                                                                                                                                      18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Raffinose synthetase; metabolism modification;
                                                                                                                                                                                        (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1999-511112/43.
                                                                                                                                         Wantanabe E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence of a raffinose synthase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97JP-0329006.
96JP-0338673.
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                                                                                                                                                                                                                                      96JP-0338673
                                                                                                                                                                                                                                                                                     97EP-0122417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            broad
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 148;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bean;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 20;
.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     food additive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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В
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Best Local S
Matches 24
                                                      Query Match
Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is the Japanese artichoke raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides in the host organism or cell is changed. Raffinose oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 36-38; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            beneficial effects on gastrointestinal flora
                                                                                                                                             The present sequence represents a raffinose synthase protein. The sequence is isolated from plant material. The protein forms raffinose by complexing alpha(1 to 6)- D-galactosyl hydroxyl group of the 6C of D-glucose residue in sucrose molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                    JP11215984-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stachys sieboldii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY30144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY30144 standard;
                                                                                                                         Sequence
                                                                                                                                                                                                                   Claim 12; Page 30-31; 40pp; Japanese
                                                                                                                                                                                                                                            New raffinose synthase gene - is prepared from a
                                                                                                                                                                                                                                                                     N-PSDB; AAZ10003.
                                                                                                                                                                                                                                                                                    WPI; 1999-511112/43.
                                                                                                                                                                                                                                                                                                            (SUMO ) SUMITOMO CHEM
                                                                                                                                                                                                                                                                                                                                        28-NOV-1997;
18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                               12-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                         10-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC 30
1 FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC 30
||||||||||| || ||:|||: ||||||
07 fgwctwdafylnvqphgvmegvqglvdggc 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                       Similarity 80.0
24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      587 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                          ΑA;
                                                                                                                                                                                                                                                                                                                                        97JP-0329006.
96JP-0338673.
                                                                                                                                                                                                                                                                                                                                                                                97JP-0342899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of a raffinose synthase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant; sucrose; raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.7%;
                                                                     80.7%;
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Pred. No. 7.1e-13;
2; Mismatches 4,
                                                         Score 146; DB 20;
Pred. No. 7.1e-13;
2; Mismatches 4
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                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 587;
                                                                                                                                                                                                                                                plant material
                                                                                      Length
                                                           Indels
                                                                                      587;
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                                                             Gaps
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RESULT 11
AAW57887
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                                                                                                                                                                                                                                                                 Ouery Match 80.7%;
Best Local Similarity 80.0%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                         The present invention relates to a mutant protein of raffinose synthas in which at least one aromatic amino acid present at the position of about 1-7 amino acids from the N-terminus is deleted or replaced. The mutant protein can be used for reducing the raffinose oilgosaccharide content in a plant body. The present protein from soybean, was used in the present invention.
                             EP849359-A2
                                                                       gastrointestinal flora; soybean.
                                                                                  Raffinose synthetase; metabolism
                                                                                                     Soybean raffinose synthetase.
                                                                                                                            23-SEP-1998
                                                                                                                                                  AAW57887;
                                                                                                                                                                     AAW57887 standard; Protein; 781 AA
                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 18-20; 30pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel mutant protein of raffinose synthase is useful for reducing the raffinose oligosaccharide content in a plant body - {\sf rag}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutant; mutein; raffinose synthase; raffinose oligosaccharide reduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soybean protein:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB98659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB98659 standard; protein;
        24-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-MAR-2001.
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DB; AAH27438.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         soybean
                                                                                                                                                                                                                                                                                                                       780 AA;
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                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                 Score 146; DB 2
Pred. No. 1e-12;
2; Mismatches
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                                                                                  modification;
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                                                                                                                                                                                                                                                                   4;
                                                                                  food additive;
                                                                                                                                                                                                                                                                                      Length 780;
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Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the soybean raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
The present sequence represents a raffinose synthase protein. The sequence is isolated from plant material. The protein forms raffinose
                                  Claim 8; Page 25-27; 40pp; Japanese
                                                                                              WPI; 1999-511112/43
                                                                                                                                          28-NOV-1997;
18-DEC-1996;
                                                                                                                                                                             12-DEC-1997;
                                                                                                                                                                                                   10-AUG-1999.
                                                                                                                                                                                                                          JP11215984-A
                                                                                                                                                                                                                                                Glycine max.
                                                                                                                                                                                                                                                                      Raffinose synthase; plant; sucrose; raffinose
                                                                                                                                                                                                                                                                                             Amino acid sequence
                                                                                                                                                                                                                                                                                                                     26-OCT-1999
                                                                                                                                                                                                                                                                                                                                           AAY30143;
                                                                                                                                                                                                                                                                                                                                                                  AAY30143 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 31-34; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oeda K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-1996;
                                                         New raffinose synthase gene - is prepared from a plant
                                                                                                                  (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SUMO ) SUMITOMO CHEM CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                             220
                                                                                                                                                                                                                                                                                                                                                                                         12
                                                                                                                                                                                                                                                                                                                                                                                                                         1998-324670/29
DB; AAV40801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                AA210002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wantanabe E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    781 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                          97JP-0329006
96JP-0338673
                                                                                                                                                                             97JP-0342899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96JP-0338673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97EP-0122417.
                                                                                                                                                                                                                                                                                             of a raffinose synthase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.7%;
                                                                                                                                                                                                                                                                                                                                                                   781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 146;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                   ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     le-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 781;
                                                          material
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RESULT 1
AAB49400
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RESULT 1
AAY32075
ID AAY3
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AC AAY3
XX
AC 17-7
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Best Local
                                                                                                                           Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                            30-APR-1999;
01-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Soybean raffinose synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB49400;
                                                                                                                                                                               The present invention provides novel plant promoters which can be used the production of transgenic plants which express genes with desired properties.
                                                                                                                                                                                                                                                                                                                                                       27-APR-2000; 2000EP-0108962
                                                                                                                                                                                                                                                                                                                                                                         02-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                         EP1048733-A2
                                                                                                                                                                                                                                                                                                                                                                                                          Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                            Plant promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB49400 standard; Protein; 781 AA.
                                                                                                                                                                                                                                     with
                                                                                                                                                                                                                                                               N-PSDB; AAC89523
                                                                                                                                                                                                                                                                                         Ishige F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC 30
|||||||||||||| ||| ||| ||| ||||
220 fgwctwdafylkvhpsgvwegvkglveggc 249
 17-JAN-2000
                  AAY32075;
                                   AAY32075 standard; Protein; 572
                                                                                                                                                               Sequence
                                                                                                                                                                                                                   Example 6; Page 24-27; 36pp; English
                                                                                                                                                                                                                                             New soybean plant promoters useful for generating transgenic plants
                                                                                                                                                                                                                                                                                                         (SUMO ) SUMITOMO CHEM CO LTD
                                                                                220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complexing alpha(1 to 6)- D-galactosyl hydroxyl group of the D-glucose residue in sucrose molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
                                                     14
                                                                              desired
                                                                                                                                                                                                                                                                         2001-104537/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                    Similarity 80.0
24; Conservative
                                                                                                                                                                                                                                                                                          Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             781 AA;
                                                                                                                                                                781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                    properties
 (first entry)
                                                                                                                                                                                                                                                                                                                            99JP-0124527
99JP-0247211
                                                                                                                                                                                                                                                                                                                                                                                                                           transgenic plant; desired property.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.7%;
                                                                                                                            80.7%;
                                                                                                                                                                                                                                                                                           0eda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 146; DB 2
Pred. No. 1e-12;
                                                                                                                    2;
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                                                                                                                             Score 146; DB 2
Pred. No. 1e-12;
                                                                                                                      Mismatches
                                                                                                                                       DB 22;
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                                                                                                                                      Length 781;
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RESULT AAY32074

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AAY32074 standard; Protein; 777

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 В
                                               Matches
                                                         Query Match
Best Local Similarity
                                                                                                                        Westar leaf cDNA by PCR. Probes or primers generated from plant raffinose synthase genes (see ANZ20207-10) may be used to obtain other raffinose synthase genes by labeled detection or amplification (claimed). These genes may be used to control the levels of raffinose produced in plants. Antisense genes can be used to knock out existing gene activity, and sense genes to increase the level of gene activity. The resulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacteria, providing general health advantages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-APR-1998;
30-APR-1998;
04-DEC-1998;
10-DEC-1998;
                                                                                                                                                                                                                                                                                                                                        New sense raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Raffinose synthase; rapeseed; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rapeseed raffinose synthase
                                                                                                                                                                                                                             This sequence represents rapessed raffinose synthase, a protein that can bind a D-galactosyl group through an alpha(1-6) bond to th hydroxy group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. cDNA (see AAZ20210) encoding the enzyme was isolated from rapessed cv. Westar leaf cDNA by PCR. Probes or primers generated from plant
                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                              Watanabe E,
                                                                                                                                                                                                                                                                                                                                                                                                                                    (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                          Sequence
 13
           1 FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC
                                                                                                                                                                                                                                                                                                                                                                                         1999-593144/51.
27; Page 36-38; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                            AAZ20210
                                                                                                                                                                                                                                                                                                                                       and antisense genes, useful for altering in food plants \mbox{\ensuremath{\text{-}}}
                                                                                                            572 AA;
                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              Oeda K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             98JP-0120550.
98JP-0120551.
98JP-0345590.
98JP-0351246.
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148
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                                                             79.6%;
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                                                 Score 144; DB 20;
Pred. No. 1.3e-12;
3; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGY"
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AAY32074;

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                                                                                                                                                                                                                                This sequence represents mustard raffinose synthase, a protein that can bind a D-galactosyl group through an alpha(1-6) bond to the hydroxy group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. cDNA (see AAZ20209) encoding the enzyme was isolated from mustard (Brassica juncea) leaf cDNA by PCR. Probes or primers generated from plant raffinose synthase genes (see AAZ20207-10) may be used to obtain other raffinose synthase genes by labeled detection or amplification other raffinose genes may be used to control the levels of raffinose produced in plants. Antisense genes can be used to knock out existing gene activity, and sense genes to increase the level of gene activity. The resulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacteria, controlling general health advantages.
                                                                                                                               Ouery Match 79.6%; Score 144; DB 20; Best Local Similarity 80.0%; Pred. No. 1.9e-12; Matches 24; Conservative 3; Mismatches 3;
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30-APR-1998;
04-DEC-1998;
10-DEC-1998;
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                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 26; Page 29-31; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New sense and antisense genes, useful for altering the level of raffinose in food plants \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAZ20209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-593144/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watanabe E, Oeda K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Raffinose synthase; mustard; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mustard raffinose synthase.
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                                                                        218
                                                                     777 AA;
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98JP-0120551.
98JP-0345590.
98JP-0351246.
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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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52 53 59
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        US-08-846-234-1
181
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Gapop 10.0 , Gapext 0.5
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R:Heck, G.R.; Dorsett, C.; Ho, T.H. submitted to the EMBL Data Library, February 1992 A;Description: Cloning and characterization of a gene, A;Reference number: S27762 A;Accession: S27762
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C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Sep-1997
C;Accession: S27762
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana A;Reference number: A85001; MUID:20083488 A;Accession: C85025 A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: cultivar C; Genetics:
A; Map position: 3
A; Introns: 64/2; 146/1; 176/2; 1
A; Note: T8H10.120
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A; Residues: 1-773 <BEN>
A; Cross-references: EMBL:AL133248
A; Cross-references: cultivar Columbia;
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R;Benes, V.; Rechmann, S.; Borkova, D.; Ansc submitted to the Protein Sequence Database, A;Reference number: Z23014
A;Accession: T46188
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-757 <HEC>
                                                                                                        hypothetical protein AT4901970 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 C;Accession: C85025 C;Accession: C85025 R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Nature 402, 769-777, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         imbibition protein homolog - Arabidopsis thaliana
N;Alternate names: protein T8HIO.120
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
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A; Introns: 64/2; 151/1; 181/2; 197/3; 489/3; 557/2
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Best Local Similarity 62.1
Matches 18; Conservative
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62.1%;
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Pred. No. 4
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; D ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E. C.A.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Vener, J.C.; Davis, R.W. A;Reference number: A86141; MUID:21016719

A;Accession: C96599
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C96599
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A; Cross-references: GB:
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein F20N2.14 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 C;Accession: C96599
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                                                                                                                                                                                                                                                                                        hypothetical protein A_IG002N01.5 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change C;Accession: T01717
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                                                                                                                                                                                                               Submitted to the EMBL Data Library, June 1997 submitted to the EMBL Data Library, June 1997 submitted to the sequence of A. thaliana IG002N01
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A; Gene: F20N2.14
A; Map position:
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A; Molecule type: DNA
A; Residues: 1-1170 <STO>
A; Map position:
A; Introns: 5/2;
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                                                                   A; Experimental source: cultivar Columbia
                                                                                           A;Cross-references: EMBL:AF007269; NID:g2191126; PID:g2191156
                                                                                                             A; Molecule type: DNA
A; Residues: 1-371 <SCH>
                                                                                                                                                          A; Status: translated from GB/EMBL/DDBC
                                                                                                                                                                            A; Accession: T01717
                                                                                                                                                                                                      A; Description: The sequence A; Reference number: 214407
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  25/3; 103/3; 126/1; 174/2; 240/1; 284/1; 295/1; 333/2; 349/2
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62.1%;
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Pred. No.
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Pred. No. 8.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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A; Note:

A_IG002N01.5

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C; Genetics:
A; Gene: VC1690
A; Map position:
                                   RESULT
S00185
                                                                                                                                                                                                                                                                                                                                                                                                                                                   fibroblast growth factor - rabbit (fragment)
c;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997
C;Accession: 146711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE004247; GB:AE003852; NID:g9656204; PIDN:AAF94840.1; GSPDB:GN001
A;Experimental source: serogroup 01; strain N16961; blotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-374 <HEI>
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Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable alpha-1,6-galactosidase VC1690 [imported] - Vibrio cholerae (strain N16961 serc
:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: E82168
                                                                                                                                                                                                                                                                  A;Cross-references: GB:L12034; NID:g165014; PIDN:AAA31248.1; PID:g165015 C;Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A; Accession: I46711
                                                                                                                                                                                                                                                                                                                                                                              A; Title: Elevated expression of basic fibroblast growth A; Reference number: I46711; MUID:93343209
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A; Residues: 1-137 <WIN>
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                                                                                                                                                                                                                                                                                                                                                                                                                 R;Winkles, J.A.; Friesel, R.; Alberts, G.F.; Janat, M.F.; Liau, Am. J. Pathol. 143, 518-527, 1993
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 N; Alternate names:
               basic fibroblast growth factor -
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nes 15; Conservative
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                                                                                                                                             3 WCTWDAFYLTVHPQGVIEGVRHLVD
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40.0%;
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Pred. No.
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No.
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RESULT
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N;Alternate names: bFGF
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 16-Jul-1999
C;Accession: A31674; S00876; S24309
R;Shimasaki, S.; Emoto, N.; Koba, A.; Mercado, M.; Shibata, F.; Cooksey, K.; Blochem. Blophys. Res. Commun. 157, 256-263, 1988
A;Title: Complementary DNA cloning and sequencing of rat ovarian basic fibro A;Reference number: A31674; MUID:89061721
A;Accession: A31674
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A;Residues: 1-146 <SIM>
C;Superfamily: fibroblast growth factor
C;Keywords: growth factor; heparin binding; mitogen
F;18-22/Region: heparin binding #status predicted
F;107-110/Region: heparin binding #status predicted
                                                                                                                                                                                                                                                         A; Decue: r--: mRNĀ
A; Molecule type: mRNĀ
A; Residues: 35-154 <ELH>
A; Cross-references: EMBL:x61697; NID:g56143; PIDN:CAA43863.1; PID:g56144
A; Cross-references: EMBL:x61697; NID:g56143; PIDN:CAA43863.1; PID:g56144
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R;El-Husseini, A.E.D.; Paterson, J.A.; Myal, Y
Biochim. Biophys. Acta 1131, 314-316, 1992
A;Tille: PCR detection of the rat brain basic
A;Reference number: S24309; MUID:92329546
A;Accession: S24309
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A;Accession: S00185
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S00185
R;Simpson, R.J.; Moritz, R.L.; Lloyd, C.J.; Fabri, L.J.; Nice, E.C.; Rubira FEBS Lett. 224, 128-132, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 16, 5201, 1988
A;Title: Nucleotide sequence of rat basic
A;Reference number: $00876; MUID:88262516
A;Accession: $00876
A;Molecule type: mRNA
A;Residues: 1-154 KUR>
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                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; translation not shown
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YCKNGGFFLRIHPDGRVDGVREKSD
                                            WCTWDAFYLTVHPQGVIEGVRHLVD 27
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Pred. No. 0.37
5; Mismatches
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Pred. No.
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56
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0.37;
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Y.; Shiu, R.P.C.
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C37360
basic fibroblast growth factor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999
C;Accession: C37360
                                                                                              A;Molecule type: protein
A;Residues: 16-35 <BER>
R;Ueno, N.; Baird, A.; Esch, F.; Ling, N.; Guillemin,
R;Ueno, L. Endocrinol. 49, 189-194, 1987
A;Title: Isolation and partial characterization of bas
A;Reference number: A61551; MUID:87162856
A;Accession: A61551
                                                                                                                                                                                                                                                                                                                       R;Bertolini, J.; Hearn, M.T.W.
Mol. Cell. Endocrinol. 51, 187-199, 1987
A;Title: Isolation, characterisation and tissue localisation A;Reference number: A61550; MUID:87247652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: pituitary gland R; Abraham, J.A.; Whang, J.L.; Tumolo, A.; Mergia, A.; Fiddes, J.C. Cold Spring Harb. Symp. Quant. Biol. 51, 657-668, 1986 A; Title: Human basic fibroblast growth factor: nucleotide sequence A; Reference number: A90924; MUID:87217066
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A; Residues: 1-154 <HEB>
A; Cross-references: GB: M30644; NID:g193296; PIDN:AAA37621.1; PID:g309239
C; Superfamily: fibroblast growth factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 3-157 <AB2>
R; Residues: 3-157 <AB2>
R; Milner, P.G.; Li, Y.S.; Hoffman, R.M.; Kodner, C.M.; Siegel, N.R.; Deuel, T.F.
Biochem. Biophys. Res. Commun. 165, 1096-1103, 1989
A; Title: A novel 17 kD heparin-binding growth factor (HBGF-8) in bovine uterus:
A; Reference number: A33784; MUID: 901212111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Abraham, J.A.; Mergia, A.; Whang, J.L.; Tumolo, A.; Friedman, J.; Hjerrild, K. Science 233, 545-548, 1986
A;Title: Nucleotide sequence of a bovine clone encoding the angiogenic protein,
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A; Experimental source: testes A; Note: this form appears to
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A;Accession: A24663
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                                                   A; Molecule type: protein
A; Residues: 27-35, 'X', 37-41 <UE3>
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A; Residues: 3-157 < ABR>
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Pred. No. 0.4;
5; Mismatches
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        basic fibroblast growth
N; Alternate names: bFGF;
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A; Molecule type: Protein
A; Molecule type: Protein
A; Molecules: 12-26 < POH>
A; Residues: 12-26 < POH>
C; Comment: The acidic and basic fibroblast growth factors are the major endothelial-c
C; Comment: The acidic and basic fibroblast growth factor
ell types in vitro (although bFGF is 30-100 times more potent than aFGF in stimulatin
C; Comment: This protein binds heparin more strongly than does aFGF.
C; Superfamily: fibroblast growth factor
C; Keywords: alternative splicing; angiogenesis; blocked amino end; growth factor; hep
C; Keywords: alternative splicing; angiogenesis; blocked amino end; growth factor; hep
F; 1-157/Product: basic fibroblast growth factor, pituitary gamma form #status experin
F; 16-157/Product: basic fibroblast growth factor, pituitary alpha form #status experin
F; 16-157/Product: basic fibroblast growth factor, hepatic form #status experimental <
F; 23-157/Product: basic fibroblast growth factor, renal form #status experimental <
F; 29-33,118-121/Region: heparin binding #status predicted
F; 4/Modified site: blocked amino end (Ala) (in mature form pituitary gamma) (probably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Note: the amino end of this form was blocked; the peptide composition ma R; Gospodarowicz, D.; Baird, A.; Cheng, J.; Lui, G.M.; Esch, F.; Bohlen, P. Endocrinology 118, 82-90, 1986
A; Title: Isolation of fibroblast growth factor from bovine adrenal gland: A; Reference number: A61094; MUID:86081530
A; Accession: A61094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 12-25,27-35,'X',37-40 <GOS>
A;Residues: 12-25,27-35,'X',37-40 delta
A;Experimental source: adrenal gland
R;Esch, F.; Baird, A.; Ling, N.; Ueno, N.; Hill, F.; Denoroy, L.; Klepper, R.; Gospod
Proc. Natl. Acad. Sci. U.S.A. 82, 6507-6511, 1985
A;Title: Primary structure of bovine pittitary basic fibroblast growth factor (FGF) a
A;Reference number: A01386; MUID:86016731
A;Accession: A01386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R:Bohlen, P.; Baird, A.; Esch, F.; Ling, N.; Gospodarowicz Proc. Natl. Acad. Sci. U.S.A. Bl., 5364-5368, 1984
A;Title: Isolation and partial molecular characterization A;Reference number: A22054; MUID:84298139
A;Accession: A22054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Experimental source: pituitary gland
R;Bahid, A.; Esch, F.; Boehlen, P.; Ling, N.; Gospodarowicz,
R;Baito, A; Esch, E.; Boehlen, P.; Ling, N.; Gospodarowicz,
Regul. Pept. 12, 201-213, 1995
A;Title: Isolation and partial characterization of an endoth
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A; Residues: 12-15
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12-157 <ESC>
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1984
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В
                    A32398
                              RESULT
                                                                                                         Matches
                                                              35 YCKNGGFFLRIHPDGRVDGVREKSD
                                                                                   WCTWDAFYLTVHPQGVIEGVRHLVD
                                                                                                                   Similarity
                                                                                                                   33.1%;
40.0%;
                                                                                                                    Score 60; I
Pred. No. 0.
                                                                                                           Mismatches
22.5K form -
h factor 2; p:
                                                                                                                              DB 1; Length 157
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factor precursor, i fibroblast growth

prostatic

growth factor;

prostat

form appears to be identical

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the

renal

form

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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 'XX', 86-88,'X', 90-91,'X', 93-95 <SH3>
A; Residues: 'XX', 86-88,'X', 90-91,'X', 93-95 <SH3>
A; Experimental source: C-Li21 hepatocellular carcinoma cell line
A; Molecule extracted from NCBI backbone (NCBIP:71595)
A; Accession: B54316
A; Molecule type: protein
A; Residues: 'XXX', 19,'X', 21-29 <SH2>
A; Note: sequence extracted from NCBI backbone (NCBIP:71594)
A; Note: sequence extracted from NCBI backbone (NCBIP:71595)
A; Note: sequence extracted from 
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A:Title: Cloning and expression of cDNA encoding human basic fibroblast growth factor.
A:Reference number: A26642; MUID:87162468

A;Accession: A26642

A;Molecule type: mRNA
A:Residues: 56-210 <KUR>
A;Cross-references: GB:M27968; NID:g182562; PIDN:AAA52448.1; PID:g182563

A;Title: Human basic fibroblast growth factor: nucleotide sequence, genomic organization A;Reference number: A90924; MUID:87217066

A;Molecule type: mRNA
A;Residues: 56-210 <ABR>
A;Molecule type: mRNA
A;Residues: 56-210 <ABR>
A;Mole: the authors translated the codon GAA for residue 108 as Gly
B;Abraham, J.A; Whang, J.L.; Tumolo, A.; Mergia, A.; Friedman, J.; Gospodarowicz, D.; Find A;Reference number: S00297; MUID:87053817

A;Accession: S00297
A;Cross-reference number: S00297; MUID:87053817
A;Mclecule type: MID:87053817
A;Mclecule type: MID:8705484
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A; Molecule type: DNA
A; Residues: 1-114 <SHI>
A; Note: authors translated the codon GGA for residue 47
A; Note: authors translated the codon KGA for residue 47
A; Note: A; Note: A; Iwane, M.; Igarashi, K.
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C;Date: 31-Jul-1989 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000
C;Date: 31-Jul-1989 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000
C;Accession: A32398; A61537; A26642; B32878; S00297; A54316; B54316; A33624; A25824; B
R;Prate, H; Kaghad, M; Prate, A.C.; Klagsbrun, M.; Lelias, J.M.; Liauzun, P.; Chalon
Proc. Natl. Acad. Sci. U.S.A. 86, 1836-1840, 1989
A;Title: High molecular mass forms of basic fibroblast growth factor are initiated by
R:Story, M.T.; Esch, F.; Shimasaki, S.; Sasse, J.; Jacobs, Blochem. Blophys. Res. Commun. 142, 702-709, 1987 A;Tille: Amino-terminal sequence of a large form of basic fa;Reference number: A25824; MUID:8715686 A;Accession: A25824
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A;Accession: A54316
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A; Residues: 1-155 <AB2>
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A; Residues: 1-210 < PRA>
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A;Accession: A32398
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A;Residues: 65-88,'X',90-98,'X',100 <GAUS
R;Sommer, A.; Brewer, M.T.; Thompson, R.C.; Moscatelli, D.; I
Blochem. Blophys. Res. Commun. 144, 543-550, 1987
A;Title: A form of human basic fibroblast growth factor with
A;Reference number: S42242; MUID:87213238
A;Accession: S42242
A;Station: S42242
                                                                                                                                                                                                               C;Keywords: alternative initiators; angiogenesis; growth factor; heparin binding; mit F;1-210/Product: basic fibroblast growth factor, 22.5K form #status predicted <MA2> F;65-210/Product: basic fibroblast growth factor, 18K form #status predicted <MAT> F;82-86/Region: heparin binding #status predicted F;171-174/Region: heparin binding #status predicted
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R; Patry, V.; Bugler, B.; Amair...
FEBS Lett. 349, 23-28, 1994
A; Title: Purification and characterization
A; Title: Purification and characterization
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A;Residues: 54-71 <PAND
R;Watson, R.; Anthony, F.; Pickett, M.; Lambden, P.; Masson,
Biochem. Biophys. Res. Commun. 187, 1227-1231, 1992
A;Title: Reverse transcription with nested polymerase chain a
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FEBS Lett. 204, 203-207, 1986
A;Title: Partial molecular characterization of endothelial cell mitogens from human b
A;Reference number: A91364; MUID:86275260
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A;Experimental source: prostate
A;Experimental source: prostate
R;Gimenez-Gallego, G.; Conn, G.; Hatcher, V.B.; Thomas,
Biochem. Biophys. Res. Commun. 135, 541-548, 1986
A;Title: Human brain-derived acidic and basic fibroblast
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A; Residues: 65-102, 'X', 104-105 <GIM>
A; Experimental source: brain
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A; Residues: 54-210 <SOM>
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Query Match 33.1%; Best Local Similarity 40.0%; Matches 10; Conservative

score 60; DB Pred. No. 0.16; Mismatches

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RESULT 2
FGF2_MOUSE
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                                              Query Match
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01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEPARIN-BINDING GROWTH FACTOR 2 PRECURSOR (HBGF-2) (BASIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GROWTH FACTOR) (BFGF) (PROSTATROPIN). FGF2 OR FGF-2.
                                                             BINDING
                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND CONCENTRATION OF THESE 2 GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE=90201563; pubMed=2318343;
Hebert J.M., Basilico C., Goldfarb M., Haub O., Martin G.R.;
Hebert J.M., Basilico Cu, Goldfarb M., Haub O., Martin G.R.;
Goldation of cDNAs encoding four mouse FGF family members and
characterization of their expression patterns during embryogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-90201563;
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PRINTS; PR00263; HBGFFGF.
ProDom; PD000831; HBGF_FGF;
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InterPro; IPR002209; HBGF_FGF.
InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
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EMBL; AF065904; AAC17504.1; -.
EMBL; AF065905; AAC17505.1; -.
EMBL; AF065905; AAC17505.1; -.
PIR; C37360; C37360.
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                                             SEQUENCE
                                                                                                                          Growth factor; Mitogen; Vascularization; Heparin-binding.
                                                                                                                                                       ProDom; PD000831; HB0 SMART; SM00442; FGF;
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HEPARIN (POTENTIAL).
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Sciurognathi; Muridae;
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Matches
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                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                            El-Husseini A.E.D., Paterson J.A., Myal Y., Shiu R.P.C.;

"PCR detection of the rat brain basic fibroblast growth factor (
mRNA containing a unique 3' untranslated region.";

Biochim. Biophys. Acta 1131:314-316(1992).

-i- FUNCTION: THE HEDARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC
IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES
VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND
CONCENTRATION OF THESE 2 GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97200905; PubMed-9048734;
Pasumarthi K.B.S., Jin Y., Cattini P.A.;
"Cloning of the rat fibroblast growth factor-2 promoter region its response to mitogenic stimuli in glioma C6 cells.";
Neurochem. 68:898-908(1997).
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MEDLINE-89061721; PubMed-3196337;
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15-JUL-1998 (Rel. 36, Last annotation update)
HEPARIN-BINDING GROWTH FACTOR 2 PRECURSOR (HBGF-2) (BASIC FIBROBLAST
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Kurokawa T., Seno M., Igarashi K.;
"Nucleotide sequence of rat basic fibroblast growth factor cDNA.";
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-!- TISSUE SPECIFICITY:
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STRAIN-SPRAGUE-DAWLEY; TISSUE-Testis;
                                 or send an email
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an email to license@isb-sib.ch).
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RESULT A FGF2_BOVIN ID FGF2_BOVIN PGF2_BOCT 93-0CT DT 23-0CT DT 23-0CT DT 23-0CT DT 23-0CT BOVIAM FACTOR GN FGF2_O OS Bost A COMMENTAL OC BOVIAM OX NCBI_T RN [2] RP SEQUEN RX MEDLIN RA ABTANA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
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InterPro: IPR002348; IL1_HBGF.
Pfam; PP00167; FGF; 1.
PR.NTS; PR00262; ILLHBGF.
PR.NTS; PR00263; HBGFFGF.
PR.NTS; PR00263; HBGFFGF; 1.
SMART; SM00442; FGF; 1.
SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF_EGF; 1.
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23-OCT-1986 (Rel. 02, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
HEPARIN-BINDING GROWTH FACTOR 2 PRECURSOR (HBGF-2) (BASIC FIBRO GROWTH FACTOR) (BFGF) (PROSTATROPIN) (CONTAINS: KIDNEY-DERIVED
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SEQUENCE
                                                                                         Esch F., Baird A., Ling N., Ueno N., Hill F., Denoroy Gospodarowicz D., Boehlen P., Guillemin R.; "Primary structure of bovine pituitary basic fibroblas (FGF) and comparison with the amino-terminal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                Abraham J.A., Mergia A., Whang J.L., Tumolo A., Hjerrild K.A., Gospodarowicz D., Fiddes J.C.; "Nucleotide sequence of a bovine clone encoding protein, basic fibroblast growth factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-86261806; PubMed-2425435;
                                                                                                                                                                                        SEQUENCE OF 10-155.
MEDLINE-86016731; PubMed-3863109;
                                                                                                                                                                                                                                                          Abraham J.A., Whang J.L., Tumolo A., Mergia A., Fiddes J.C.
"Human basic fibroblast growth factor: nuclectide sequence,
organization, and expression in mammalian cells.",
Cold Spring Harb. Symp. Quant. Biol. 51:657-668(1986).
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-87217066; PubMed-3472745;
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
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    SEQUENCE OF 1-9
                                                                        acidic
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A31674; A31674.
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U78079; AAC53225.1;
X61697; CAA43863.1;
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Pred. No. 0.18;
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PIR; A24663; GKBOB.

PIR; A24819; A24819

PIR; A32878; A32878

PDB; 1BAS; 31-CCT-93.

InterPro; IPRO02209; HBGF_FGF.

InterPro; IPRO02348; IL1_HBGF.

Pfam; PF00167; FGF; 1.

PRANTS; PR00262; IL1HBGF.

PRINTS; PR00263; HBGF_FGF.

PRODOm; PD000831; HBGF_FGF; 1.

SMART; SM00442; FGF; 1.
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MEDLINE-91095983; PubMed-1702556;
MEDLINE-0105983; PubMed-1702556;
ACM X. Komiya H., Chirino A., Faham S.,
HSu B.T., Rees D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-87119165; PubMed-3809608;
Ueno N., Baird A., Esch F., Shimasaki S., Ling N., Guillemin R.;
"Purification and partial characterization of a mitogenic factor
bovine liver: structural homology with basic fibroblast growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Regul.
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MEDLINE-86095426; PubMed-4081126;
BAITI A., Esch F., Boehlen P., Ling N., Gospodarowicz D.;
"Isolation and partial characterization of an endothelial cell factor from the bovine kidney: homology with basic fibroblast factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-86295737; PubMed-3741423; Ueno N., Baird A., Esch F., Ling "Isolation of an amino terminal e growth factor.";
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Growth factor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 251:90-93(1991)
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                                                                                                                                   3D-structure.
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                                                                                                                                                                                                                                                                                                                                                    send an email to license@isb-sib.ch).
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                                        CELL ATTACHMENT SITE (POTENTIAL)
CELL ATTACHMENT SITE (POTENTIAL)
HEPARIN (POTENTIAL).
HEPARIN (POTENTIAL).
                                                                                             KIDNEY-DERIVED GROWTH FACTOR.
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Best Local S
Matches 10
                                                                                                                                     SEQUENCE FROM N.A.

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MEDLING-87217066; PubMed-3472745;

Abraham J.A., Whang J.L., Tumolo A., Mergia A., Fiddes J.C.;

Abraham J.A., Whang J.L., Tumolo A., Mergia A., Fiddes J.C.;

Pluman basic fibroblast growth factor: nucleotide sequence,

"Human basic fibroblast growth factor: nucleotide sequence,

organization, and expression in mammalian cells.";

organization, and expression in mammalian cells.";
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01-NOV-1988 (Rel. 09, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HEPARIM-BINDING GROWTH FACTOR 2 PRECURSOR (HBGF-2) (BASIC FIBROBLAST GROWTH FACTOR) (BFGF) (PROSTATROPIN).
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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                                                         Sommer A.,
Rifkin D.B
                                                                                           SEQUENCE FROM N.A. MEDLINE=87213238;
                                                                                                                                                                                                                                                                            "Human basic fibroblast growth factor: nucleotide sequence and genomic organization."; EMBO J. 5:2523-2528(1986).
                                                                                                                                                                                                                                                                                                                               Abraham J.A., Whang J.L., Tumolo Gospodarowicz D., Fiddes J.C.;
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=87053817; PubMed=3780670;
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                      terminus.";
                                       ot human
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                                                                      213238; PubMed=3579930; Brewer M.T., Thompson
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Primates;
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40.0%;
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SEQUENCE FROM N.A.
MEDLINE-87162468; PubMed-2435575;
Kurokawa T., Sasada R., Iwane M., Igarashi K.;
Kurokawa -- expression of cDNA encoding human
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MEDLINE-87156686; PubMed-2435284;
Story M.T., Esch F., Shimasaki S., Sasse J., Jacobs S.C., Lawson R.K Story M.T., Esch F., Shimasaki S., Sasse J., Jacobs S.C., Lawson R.K "Amino-terminal sequence of a large form of basic fibroblast growth factor isolated from human benign prostatic hyperplastic tissue.";
                                                                                                                                                                                                                      MEDLINE-91195368; PubMed-1849658; Shang J., Cousens L.S., Barr P.J., Sprang S.R.; Three-dimensional structure of human basic fibroblast a structural homolog of interleukin 1 beta."; proc. Natl. Acad. Sci. U.S.A. 88:3446-3451(1991).
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MEDLINE=89184522; PubMed=2538817;

Prats H., Kaghad M., Prats A.C., Klagsbrun M., L

Prats H., Kaghad M., Tauber J.P., Amalric F.,

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Hsu B.T., Rees D.C.
"Three-dimensional
                                                                                                                      Ago H., Kitagawa Y., "Crystal structure of resolution.";
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MEDLINE=86275260; PubMed-3732516;
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MEDLINE=94004464; PubMed=7691311;
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MEDLINE-91195367; PubMed-1707542;
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                                                           MEDLINE=91095983; PubMed=1702556;
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                                               Chirino A.,
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EMBL; M17599; AAA52534.1; ALT_INIT.
EMBL; X04431; CAA280027.1; -.
EMBL; X044432; CAA28028.1; -.
EMBL; X04433; CAA28029.1; -.
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-! FUNCTION: THE HEPARIN-BINDING FOR A VARIETY OF CELL TYPES I IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES I VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND CONCENTRATION OF THESE 2 GROWTH FACTORS.

-!- SUBUNIT: MONOMER.

-! SUBUNIT: MONOMER.
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Pfam; PF00167; FGF; 1.
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                                                                                                                                                             Growth factor; Mitogen;
                                                                                                                                                                         SMART; SM00442; FGF; PROSITE; PS00247; HBC
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S00297; S00297
4FGF; 15-APR-92
4FGF; 15-JUL-93
1FGA; 15-JUL-93
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Simpson R.J., Moritz R.L., Lloyd C.J., Fabri L.J., Nice E.C.
Rubira M.R., Burgess A.W.;
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Sutton R., Ward W.G., Re
Submitted (SEP-1994) to
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.
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                                                                                                               SUBUNIT: MONOMER.
MISCELLANEOUS: THIS
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Pfam; PF00167; FGF; 1.
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KUSEWITT D.F., Sabourin C.L.K., Sherburn T.E., Ley R.D.;

"Characterization of cDNA encoding basic fibroblast growth factor the marsupial Monodelphis domestica.";

DNA Cell Biol. 13:549-554(1994);

-:- FUNCTION: THE HEBARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND CONCENTRATION OF THESE 2 GROWTH FACTORS.
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01-FEB-1996 (Rel. 33, Created)
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01-FEB-1997 (Rel. 35, Last annotation update)
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HEPARIN-BINDING GROWTH FACTOR 2 PRECURSOR (HB
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                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outstati the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
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Mammalia; Metatheria; Didelphimorphia; Didelphidae;
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Best Local S
Matches 9
SUA_ECOLI
SIMA_ECOLI
SUA_ECOLI
P75853; Q9R7Q5;
15-JUL-1998 (Rel. 36, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMedt G. III, Bloch C.A.,
Blattner F.R., Plunkett G. III, Bloch C.A.,
Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., RC
Riley M., Collado-Vides J., Glasner J.D., RC
Riley M., Collado-Vides J., Kirkpatrick H.A., Gof
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BINDING
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SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF_FGF; 1.
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PRINTS; PR00262; IL1HBGF
PRINTS; PR00263; HBGFFGF
                                                                                                                                                                                                                                                                                                                      Teisinger T.;
"The Escherichia coli ssuEADCB gene cluster is required utilization of sulfur from aliphatic sulfonates and is the transcriptional activator Cbl.";
J. Biol. Chem. 274:29358-29365(1999).
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                                                                                                            Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Oshima T., Aiba H., Baba T., Fujita K., Kanai K., Kashimoto K., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Kimura S., Kitagawa M., Makino K., Mashimoto H., Nishio Y., Saito N.
                                                                                                                                                                                                          Science
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli
                                                                                                                                                           MEDLINE=97061202; PubMed=8905232;
                                                                                                                                                                       STRAIN-K.
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                         "The complete genome sequence Science 277:1453-1474(1997).
                                                                                                                                                                                                                                  Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99436146; PubMed=10506196;
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9; Conserv
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BY SIMILARITY
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Pred. No. 0.25
6; Mismatches
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HEPARIN (POTENTIAL)
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                               PROTEIN.
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C., Yamamoto
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Best Local
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2_CHICK
FGF2_CHICK
P48800;
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FGF2 OR FGF-2.
Gallus gallus (Chicken).
Gallus gallus (Chicken).
Gukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae; Phasianinae;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                               Borja A.Z., Zeller R., Meijers C.;

"Expression of alternatively spliced bFGF first coding exons and antisense mRNAs during chicken embryogenesis.";

Dev. Biol. 157:110-118(1993).

-1- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND CONCENTRATION OF THESE 2 GROWTH FACTORS.

-1- SUBUNIT: MONOMER.

-1- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY THAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
HEPARIN-BINDING GROWTH FACTOR 2 PRECURSOR (HBGF-2) (BASIC FIBROBLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL: AJ237695; CAB40390.1; -.
EMBL: AE000195; AAC74022.1; ALT_INIT.
EMBL: D90732; BAAA35691.1; ALT_INIT.
ECOGene; EG13707; 88UA.
InterPro; IPR001638; SBP_bac_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GROWTH FACTOR) (BFGF).
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                            EMBL; M95707; AAA48617.1;
HSSP; P09038; 1BFF.
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   InterPro;
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Portential.
1 21 POTENTIAL.
22 319 POTETIVE ALIPHATIC SULFONATES
PROTEIN.
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A PEAMTS; PF0016; ILIN_
PRINTS; PR00262; ILIN_
DR PRINTS; PR00263; HBGFFGF; 1.

PRODOMS; PR00263; HBGF_FGF; 1.

DR SMART; SM00442; FGF; 1.

DR SMART; SM00442; FGF; 1.

DR PROSITE; PS00247; HBGF_FGF; 1.

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        HSSP; P18052; 1YFO.

F1yBase; FBgn0014007; Ptp69D.

InterPro; IPR001777; FN_III.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003598; Ig_c2.

InterPro; IPR003600; Ig_like.

InterPro; IPR00387; TYR_phosphatase.

InterPro; IPR000242; Tyr_prot_phphtase.
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P16620;
01-AUG-1990
01-AUG-1990
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       + +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).
-i- FUNCTION: IT IS POSSIBLE THAT DPTP IS A CELL ADHESION RECEPTOR
-i- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=90046860; PubMed=2554325;

Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;

"A family of receptor-linked protein tyrosine phosphatases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygotta; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYROSINE-PHOSPHATE PHOSPHOHYDROLASE). PTP69D OR DPTP.
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01-AUG-1990 (Rel. 15, Last sequence update)
20-AUG-2091 (Rel. 40, Last annotation update)
PROTEIN-TYROSINE PHOSPHATASE DPTP PRECURSOR (EC 3.1.3.48) (PROTEIN-
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                                                                                                                                                                                                                                                                                                                          tities requires a license agreement (See send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: CONTAINS 2 IMMUNGGLOBULIN-LIKE C2-TYPE DOMAINS.
SIMILARITY: CONTAINS 2 FROMECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
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9; Conservative
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s; Brachycera;
                                                                                                                                                                                                                                                                                                                                                         http://www.isb-sib.ch/announce/
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Best Local
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P11319;
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01-JUL-1989 (
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SEQUENCE
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SMART; SM00060; FN3; 3.
SMART; SM00408; IGC2; 1.
SMART; SM00410; IG_11ke; 1.
SMART; SM00194; PTPC; 2.
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DOMAIN
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                                                                        01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
PROBABLE EARLY E3 12.1 KDA GLYCOPROTEIN.
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SEQUENCE FROM N.A
                                           Human adenovirus type 3. Viruses; dsDNA viruses,
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PF00102; Y_phosphatase;
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8; Conserv
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PS50055; TYR_PHOSPHATASE_7; 2.
PS50055; TYR_PHOSPHATASE_PTP; 2.
PS50055; TYR_PHOSPHATASE_PTP; 2.
PS50055; TYR_PHOSPHATASE_PTP; 2.
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                                            no RNA stage; Adenoviridae;
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MW; F809
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PROTEIN-TYROSINE PHOSPI
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P42786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria
Bacteria;
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01-NOV-1995 (Rel. 32, L
20-AUG-2001 (Rel. 40, L
PROLINE IMINOPEPTIDASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Region E3 of human adenoviruses; differences between adenovirus-3 and the non-oncogenic adenovirus-2.";
                                                                                                                         use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                        the
                                                                                                                                                                                                                                                                  Mol. Microbiol. 9:1203-1211(1993).
1- FUNCTION: HYDROLYSES PEPTIDES HAVING THE STRUCTURE PRO-Y-Z-YIELD FREE PROLINE. ALSO HYDROLYSES THE DIPEPTIDE PRO-GLY.
-1- CATALYTIC ACTIVITY: RELEASE OF A N-TERMINAL PROLINE FROM A
                                                                                                                                                                                                                                                                                                                                                 Albertson N.H., Koomey M.; "Molecular cloning and characterization of a proline iminopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dId
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CARBOHYD 77 77
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                                                                                           or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                               from Neisseria gonorrhoeae
                                                            Z25461; CAA80948.1;
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Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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STRAIN-K12 / W3110;
STRAIN-K12 / W3110;
STRAIN-K12 / W3110;
Takemoto K., Mori H., Miki T., Hatada E., Fukuda R., Ichihara S., Yamamoto Y., Inokuchi H., Miki T., Hatada E., Fukuda R., Ichihara S., Mizuno T., Makino K., Nakata A., Yura T., Sampei G., Mizobuchi K.;

*Systematic sequencing of the Escherichia coli genome: analysis of the 4.0 - 6.0 min (189,987 - 281,416bp) region.";
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ACT_SITE
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MEDLINE-97426617; PubMed-9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
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P31546;
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                                                                                             Ohnishi M., Murata T., Nakayama K., Kuhara S.,
Kurokawa K., Yasunaga T., Makino K., Shinagawa
                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-0157:H7 / R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science
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SEQUENCE FROM
                                   "Development of primer sets for direct sequence the ribosomal operons of Escherichia coli."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ date of the EMBL/GenBank/DBJ date of the EMBL/GenBank/DDBJ date of the EMBL/G
                                                                                                                                                                                                                                      Davis K., Federspiel
Lashkari D., Lew H.,
                                                                                                                                                                                                                                                                                  Schramm S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
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H., Hayashi
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RX MEDLINE-21156231; PubMed-11258796;

RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama R. Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama R. Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Ra Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T. Ruhara S., Shiba T., Hattori M., Shinagawa H.;

Ruhara S., Shiba T., Hattori M., Shinagawa H.;

Ruhara S., Shiba T., Hattori M., Shinagawa H.;

Ruhara S., Shiba T., Hattori M., Shinagawa H.;

Ruhara S., Shiba T., Hattori M., Shinagawa H.;

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"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
                                   SEQUENCE FROM N.A. MEDLINE-97061201; Po Kaneko T., Sato S.,
                                                                                                                        NCBI_TaxID=1148; (1]
                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence up
20-AIG-2001 (Rel. 40, Last annotation
LIPOATE-PROTEIN LIGASE B (EC 6.-..-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      P74519;
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Hypothetical protein; Complete
SEQUENCE 191 AA; 21294 MW;
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L; AE000129; AAC73311.1; -.
L; D83536; BAA77877.1; -.
L; U70214; AAB08628.1; -.
L; AB035926; BAA93568.1; -.
L; AE0051595; AAC54502.1; -.
L; AP002550; BAB33625.1; -.
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Kotani H.,

Tanaka

A., Asami Sasamoto

Asamizu E., amoto S., Ki

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ID YIALP
AC P18205
DT 01-NOV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P18205;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
HYPOTHETICAL 21 KDA PROTEIN IN INALL 5'REGION (ORF 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: INVOLVED IN THE ATTACHMENT OF LIPOYL GROUPS TO PROTEINS,
                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                       savastanoi.";
proc. Natl. Acad. Sci. U.S.A. 87:5797-5801(1990).
-i- FUNCTION: MAY BE A MEMBRANE-BOUND PROTEIN, POSSIBLY INVOLVED
IN IAA OR IAA-LYSINE TRANSPORT.
                                                                                                                                                                                                                                                       Roberto F., Klee H., White F., Nordeen R., Kosuge T.; "Expression and fine structure of the gene encoding N epsilon-(indole-3-acetyl)-L-lysine synthetase from Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas syringae (pv. savastanoi)
Plasmid pIAA1.
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PROSITE; PS01313; LIPB; 1.
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                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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LIPOIC ACID TO THE EPSILON-AMINO GROUP OF A SPECIFIC LYSINE
RESIDUE IN LIPOYLATED PROTEINS (BY SIMILARITY).
PATHWAY: LIPOATE BIOSYNTHESIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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PIR; B35961; B35961.
InterPro; IPR002528; UPF0013.
Pfam; PF01554; UPF0013; 1.
Hypothetical protein; Transport; Plasmid.
SEQUENCE 302 AA; 32450 MW; 15728E0CE5
201 FAFCRWGGALDAHRAAIHCHLSLPQYGATGVRHTV 235
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                          1 FGWCTW----DAFYLTVH-----PQGVIEGVRHLV 26
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                                                                     26.8%;
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sp_organelle:*
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sp_human:*
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sp_bacteria:*
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sp_unclassified:*
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Q43408
Q43466
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Q40077
Q9SCM1
Q9SYJ4
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Q9FND9
        Q60487
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                                                                                    Q9M4M7
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     Q9m4m7 persea amer
Q91fz7 arabidopsis
Q04607 arabidopsis
Q04607 arabidopsis
Q9krf2 vibrio chol
Q00527 homo sapien
Q16443 homo sapien
Q77767 canis famil
P78443 homo sapien
Q21801 caenorhabdi
Q60487 cavia porce
                                                                 09zt62 cucumis sat
09fnd9 arabidopsis
09sbz0 phaseolus a
043408 brassica ol
039466 cicer ariet
040077 hordeum vul
09scm1 arabidopsis
09sty4 arabidopsis
09sty4 arabidopsis
09467 arabidopsis
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crassostrea
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49	49	49	49	49	49.5	50	50	50	50	51	51	51	51	51	51	52	52	52	52	52.5	۲.	53	54	54	54
27.1	27.1		27.1		27.3		27.6	27.6	27.6	28.2	28.2	28.2	28.2	28.2	28.2	28.7	28.7	28.7	28.7	29.0	29.0	29.3	29.8	29.8	29.8
321	293	180	80	80	352	417	386	381	284	1039	989	417	283	106	106	1428	619	619	237	265	265	557	489	390	390
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Q9h1x0 homo sapien		Q9kx15 streptomyce	Q27313 plasmodium	Q26176 plasmodium	Q9gyll leishmania		Q9ajd7 kitasatospo	Q9xuv4 caenorhabd1	Q914i3 salmonella	O23461 arabidopsis		Q9fxt4 oryza sativ	Q9fvm2 arabidopsis	Q83124 mastadenovi	Q83115 mastadenovi	Q9vu03 drosophila		Q9z935 chlamydia p	Q9c7n3 arabidopsis	Q9htb8 pseudomonas	P72162 pseudomonas	Q9keu2 bacillus ha		Q43811 pelargonium	Q43812 pelargonium

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-LEAF;
Ohsumi C., Nozaki J., Kida T.;
Ohsumi C., Nozaki J., Kida T.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF073744; AAD0283z.1; -.
Transferase; Glycosyltransferase.
SEQUENCE 784 AA; 86919 MW; 3B06A491F0908933 CRC64;
Q9FND9 PRELIMINARY; PRT; 78
Q9FND9;
Q1-MAR-2001 (TIEMBLIEL. 16, Created)
Q1-MAR-2001 (TIEMBLIEL. 16, Last sequen)
Q1-MAR-2001 (TIEMBLIEL. 16, Last annota
RAFFINOSE SYNTHASE PROTEIN.
Arabidopsis thaliana (Mouse-ear cress).
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.

NCBI_TaxID-3659;
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092T62;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RAFFINOSE SYNTHASE (EC 2.4.1.82).
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Q1-NOV-1996 (TrEMBLrel. 12, Last se
Q1-NOV-1999 (TrEMBLrel. 12, Last ar
PUTATIVE IMBIBITION PROTEIN.
Brassica oleracea (Cauliflower).
Fukaryota; Viridiplantae; Streptop
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLING-20117502; PubMed-10652123;

Peterbauer T., Mucha J., Mayer U., Popp M., Gloessl J., Richter A.;

"Synthesis of stachyose in seeds of adzuki bean (Vigna angularis).

Molecular cloning and functional expression of stachyose synthase f adzuki bean.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY 2000 (TrEMBLrel. 13, Last sequence update)
01-MAR 2010 (TrEMBLrel. 16, Last annotation update)
01-MAR 2011 (TrEMBLrel. 16, Last annotation update)
GALACTINOL-RAFFINOSE GALACTOSYLTRANSFERASE (EC 2.4.1.67).
Phaseolus angularis (Adzuki bean) (Vigna angularis).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid.
eurosids I; Fabales; Fabaceae; Papillonoideae; Vigna.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structural analysis of Arabidopsis thaliana chromosome Sequence features of the regions of 1,044,062 bp covered physically assigned P1 clones."; DNA Res. 4.291-300(1997).
EMBL; AB006702; BAB11595.1; -
SEQUENCE 783 AA; 86237 MW; 3C37D1D7871888AC CRC64;
                                                                                                               Q43408
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EMBL; Y19024; CAB64353.1; -.
Transferase; Glycosyltransferase.
SEQUENCE 857 AA; 94949 MW; 85248C4B81165679 CRC64;
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01-MAY-2000
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    Magnoliophyta; eudicotyledons;
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edons; core eudicots; Rosic
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01-NOV-1996
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Q39466;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
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SEQUENCE 765 AA; 84084 MW; 73398603048E9B58
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NCBI_TaxID=3712;
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Eukaryota; Viridiplantae; Streptophyta
Spermatophyta; Magnoliophyta; eudicoty
eurosids I; Fabales; Fabaceae; Papillio
Heck G.R.,
Submitted
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SEQUENCE FROM N.A.
                                                                                                                            Spermatophyta; Magnoliophyta; Liliopsida; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cervantes
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                                                                                                                                                                                                          Hordeum vulgare (Barley).
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                        SIP1.
                                                                                                                                                                                                                                                                                                    SEED IMBIBITION
                                                                                                                                                                                                                                                                                                                                01-NOV-1996
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                        SEQUENCE FROM N.A.
                                                                                                                NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31
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18; Conser
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357
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39465 MW;
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?5.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 108; DB
; Pred. No. 5.2e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
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Pred.
      EMBL/GenBank/DDBJ
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                                                                                                                                                                                 Embryophyta; Tracheophyta;
a; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ນ. 2e-07;
7;
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Matches
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SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Huang E.N., Nascimento L., de la Bastide M., Habermann K., Vil M.D.,
Preston R.R., Spiegel L.A., See L.H., Shah R., Matero A.,
O'Shaughnessy A., Rodriguez M., Shekher M., Swaby I., Schutz K.,
Parnell L.D., Dedhia N.N., McCombie W.R.;
Parnell L.D., Dedhia N.N., McCombie W.R.;
"Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 cM.";
"Arabidopsis thaliana BAC T811 from chromosome IV near 10 cM.";
                                                                                                                                                                                                                                                        Q9SYJ4 PRELIMINARY; PRT; 807 AA.
Q9SYJ4;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2000 (TrEMBLrel. 15, Last annotation update)
Q1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
PUTATIVE RAFFINOSE SYNTHASE OR SEED IMBIBITION PROTEIN.
T7B11.23 OR A74G01970.
ARABIdopsis thaliana (Mouse-ear cress).
Eukaryota; V1ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9SCM1 PRELIMINARY;
Q9SCM1;
01-MAY-2000 (TTEMBLIFEL 13,
01-MAY-2000 (TTEMBLIFEL 13,
01-MAY-2000 (TTEMBLIFEL 13,
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Benes V., Rechmann S.,
Mayer K.F.X., Quetier F
Submitted (NOV-1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo; Spermatophyta; Magnollophyta; eddicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis sequencing project;
bmitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
BL; AL133248; CAB66109.1; -.
QUENCE 773 AA; 85143 MW; 0852F9E67952C8D3 CRC64;
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AA; 82133
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F., Salanoubat M.;
o the EMBL/GenBank/DDBJ (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 :
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Pred. No. 1.2e-06;
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udicots; Rosidae;
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Q9LF27;
Q9LF27;
01-OCT-2000
01-OCT-2000
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Q9M4M7;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
PUTATIVE SEED IMBIBITION PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide
Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodri
Shekher M., Schutz K., See L.H., Swaby I., Habermann K.,
Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                  F20N2.14.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheopsermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
EMBL; AC007138; AAD22659.1; -
EMBL; AL161193; CAB80690.1; -
SEQUENCE 807 AA; 90122 MW; 963DCD5A827B336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Merodio C., Grierson D.;
"Isolation and characterization of cDNAs for mRNAs regulated "Isolation and characterization of cDNAs for mRNAs regulated cold storage of avocado (Persea americana Mill.) fruit.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ133148; CAB77245.1; -.

SEQUENCE 779 AA; 85368 MW; C3A8B43160316785 CRC64;
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Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Laurales;
NCBI_TaxID=3435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIP.
   NCBI_TaxID=3702;
[1]
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SEQUENCE FROM N.A.
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vans A.D., Dopico B., I
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58.6%;
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2; Mismatches
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Pred. No. 1.2e-05
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Submitted
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EMBL; AC002328; AAF79504.1; -. SEQUENCE 1170 AA; 129057 MW; 98B43A04E3F66D44 CRC64;
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Shinn P.P., Buehler E.E., Dunn P.P., Feng J.J., Kim C.C., Li Y.Y.
Shinn P.P., Buehler E.E., Dunn P.P., Feng J.J., Kim C.C., Li Y.Y.
Walker M.M., Altafi H.H., Araujo R.R., Conn L.L., Conway A.A.B.,
Gonzalez A.A., Hansen N.N.F., Huizar L.L., Kremenetskaia I.I.,
Lenz C.C., Li J.J., Liu S.S., Luros S.S., Rowley D.D., Schwartz of the Lambert S.S., Property J. S., Laros S.S., Rowley D.D., Schwartz of Toriumi M.M., Vysotskaia V.V., Yu G.G., Davis R.R.W.,
Federspiel N.N.A., Theologis A.A., Ecker J.J.R.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                               01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
SIMILAR TO SEED IMBIBITION PROTEIN.
A_IG002N01.5.
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                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streed, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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               STRAIN-CV.
                                SEQUENCE FROM N.A.
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Pred. No.
                                                                                                                                                                                                                                                       PRT;
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                                                                 01-JAN-1998 (TremBLrel. 05, Created)
01-JAN-1999 (TremBLrel. 09, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation updat
BASIC FIBROBLAST GROWTH FACTOR (FRAGMENT).
FGF-2 OR FGF2.
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STRAIN=EL TOR N16961 / SEROTYPE 01;

WEDLINE=20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M. Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Dodson R.J., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Selle McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter Fraser C.M.;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-OCT-2000 (TrEMBLrel. 15, Last annotation
ALPHA-1,6-GALACTOSIDASE, PUTATIVE.
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01-OCT-2000
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Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "DNA sequence of both chromosomes cholerae.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 374 AA;
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TIGR; VC1690; -
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EMBL; AE004247; AAF94840.1;
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    Chordata;
Primates;
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Pred. No. 0.62
4; Mismatches
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Pred. No.
       Craniata; V
Catarrhini;
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0.056;
                            Vertebrata; Euteleostomi;
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       Hominidae;
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NCBI_TaxID=9606; EQUENCE FROM N.A.

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutations in the 5' untranslated region of the FGF-2 gene: transition G to A on position 19 and transversion G to C on position 97."; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases. EMBL; Y13468; CAA73868.1; -.
                                                                                                                                                                          "Basic fibroblast growth factor gene exp
Ann. N. Y. Acad. Sci. 638:109-126(1991).
EMBL; S81809; AABZ1432.2; ...
HSSP; P09038; 1BFF.
                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Handschug K., Glaeser C.; "Polymorphism in the 5' untranslated region of the FGF-2 gene: C transition (79 bp upstream of the first CTG codon)."; Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                         Pfam; PF00167; FGF; ProDom; PD000831; H
                                                                                                                                                                                                                           Florkiewicz R.Z., Shibata F., Barankiewicz T., Baird Gonzalez A.M., Florkiewicz E., Shah N.;
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Pfam; PF00167; FGF; 1.
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                                                                                                                                                                InterPro; IPR002209; HBGF_FGF.
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YCKNGGFFLRIHPDGRVDGVREKSD
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llarity 40.0%;
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11670 MW;
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Last annotation update)
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Pred. No.
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112
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TYPE TOLE BYGF IN CANINE HEMBINGIOSETCOMB.";

RI TUDE TOLE BYGF IN CANINE HEMBINGIOSETCOMB.";

RI SUBMITTED (APPR-1998) to the EMBL/GENBAK/DDBJ databases.

RI SUBMITTED (APPR-1998) to the EMBL/GENBAK/DDBJ databases.

RI SUBMITTED (AND TUDE SPECTRUM MITOGENIC, AND NEUROTROPHIC FOR PROCESSES, INCLUDING LIMB DEVELOPMENT, AND GLOGENESIS, WOUND DEPROCESSES, INCLUDING LIMB DEVELOPMENT, AND GLOGENESIS, WOUND CHEALING, AND TUMOR GROWTH. POTENT MITOGEN AND CHEMOATTRACTANT FOR MESENCHYME-DERIVED CELLS. IMPLICATED IN THE DIFFERENTIATION,

COMESSENCHYME-DERIVED CELLS. IMPLICATED IN THE DIFFERENTIATION,

COMESSENCHYME-DERIVED CELLS. IMPLICATED IN THE CENTRAL NERVOUS CONSTRUCTION.

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CONSTRUCTION.
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InterPro; IPR002209; HBGF_FGF.
InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
PRLNTS; PR00262; IL1HBGF.
ProDom; P0000831; HBGF_FGF; 1.
SMART; SM00442; FGF; 1.
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PRELIMINARY; PRT; 130 AA.
077767;
01-NOV-1998 (TrEMBLrel. 0B, Created)
01-NOV-1998 (TrEMBLrel. 0B, Last sequence update)
01-NOV-1998 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BASIC FIBROBLAST GROWTH FACTOR (BFGF) (FGF-2) (HEPARIN-BINDING GROWTH FACTOR 2) (HBGF-2) (PROSTATROPIN) (PROSTATIC GROWTH FACTOR)
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SEQUENCE
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Growth factor; Mitogen; Vascularization; Heparin-binding;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
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3: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*

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1 FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC 30	Query Match Best Local Similarity 100.0%; Score 181; DB 4; Length Best Local Similarity 100.0%; Pred. No. 3.9e-20; Matches 30; Conservative 0; Mismatches 0; Indels		COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC COMPOTER: SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/846,234 FILING DATE:	CORRESPONDENCE ADDRESS: ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR CITY: ARLINGTON STATE: VIRGINIA COUNTRY: USA	ESULT 1 S-08-846-234-1 Sequence 1, Application US/08846234 Patent No. 6166292 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: NOZAKI Jinshi APPLICANT: KIDA Takao TITLE OF INVENTION: RAFFINOSE SYNTHASE GENE, METHOD FOR TITLE OF INVENTION: RAFFINOSE, AND TRANSGENIC NUMBER OF SEQUENCES: 22		60 33.1 150 5 PCT-US95-09172-8 60 33.1 153 3 US-08-325-186-2 60 33.1 154 2 US-08-438-439C-24 60 33.1 154 3 US-08-325-186-1 60 33.1 154 5 PCT-US91-02186-6 60 33.1 155 1 US-07-959-369-7 60 33.1 155 1 US-08-023-757-2 60 33.1 155 1 US-08-023-757-4 60 33.1 155 1 US-08-023-757-4 60 33.1 155 1 US-08-023-757-4 60 33.1 155 1 US-08-177-502-2 60 33.1 155 1 US-08-177-502-4 60 33.1 155 1 US-08-177-502-4 60 33.1 155 1 US-08-439-725A-10 60 33.1 155 2 US-08-867-471-10 60 33.1 155 2 US-08-867-471-10 60 33.1 155 6 5514566-8
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RESULT 2
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 784 amino acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-413-3000
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APPLICANT: KIDA Takao
TITLE OF INVENTION: RAFFINOSE SYNTHASE GENE, METHOD FOR
TITLE OF INVENTION: PRODUCING RAFFINOSE, AND TRANSGENIC PLANT
                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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COUNTRY:
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ZIP: 94304-1018
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                                                                                                                                                                              Palo Alto
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                                                                                                                                                                                                                    755 Page Mill Road
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TD NO: 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    CARRILLO, PEDRO A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OLSEN, DAVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZHANG, SUNNY
OLSON, PAMELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MASCARENHAS, DESMOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OSUMI Chieko
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C
55 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 181; DB 4
100.0%; Pred. No. 2e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08284784 Patent No. 5629172
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Best Local
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: 221
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                 REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: PARK, FREDDIE K.
REGISTRATION NUMBER: 35,6
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: OLSEN, DAVID R.
APPLICANT: CARRILLO, PEDRO A.
TITLE OF INVENTION: EXPRESSION OF FUSION POLYPEPTIDES
TITLE OF INVENTION: TRANSPORTED OUT OF THE CYTOPLASM WITHOUT LEADER SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MASCARENHAS, DESMOND
                                                                                                                                                                           APPLICATION NUMBER: US/08/284,784 FILING DATE: 02-AUG-1994 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 02-AUG-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                     STREET: 755 Page I
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 YCKNGGFFLRIHPDGRVDGVREKSD 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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                                                   TELEFAX:
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10; Conservative
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(415) 494-0792
                                                                                                                                                                                                                                                                                                                                                        USA
                                                   (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OLSON, PAMELA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZHANG, YANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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40.0%;
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                                                                                                           22095-20275.20
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Best Local Similarity 40.0%;
Matches 10; Conservative
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                                                    Matches
                                                                                   Query Match
                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,811
FILING DATE: 12-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/284,784
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/100,744
FILING DATE: 02-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Zhang, Yang
APPLICANT: Olson, Pamela S.
APPLICANT: Olsen, David R.
APPLICANT: Cohen, Pedro A.
APPLICANT: Cohen, Pedro A.
TITLE OF INVENTION: EXPRESSION OF FUSION POLYPEPTIDES
TITLE OF INVENTION: TRANSPORTED OUT OF THE CYTOPLASM WITHOUT LEADER
TITLE OF INVENTION: SEQUENCES
                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
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CORRESPONDENCE ADDRESS:
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10 YCKNGGFFLRIHPDGRVDGVREKSD 34
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STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                  NAME: Buffinger, Nicholas S
REGISTRATION NUMBER: 39,124
REFERENCE/DOCKET NUMBER: 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 755 PAGE
CITY: Palo Alto
                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                   Local Similarity les 10; Conserv
3 WCTWDAFYLTVHPQGVIEGVRHLVD 27 :| |:| :|| | :|| |
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755 PAGE MILL ROAD
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                                                    Conservative
                                                                                                                                                          linear
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FastSEQ for Windows Version 2.0b
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                                                                   Score 60; DB 2
Pred. No. 0.13;
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Pred. No. 0.13;
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                                                   Mismatches
                                                                                     DB 2;
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Best Local Similarity 40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (619)552-0095
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                    APPLICANT: Garofano, Luisa
APPLICANT: Battistini, Carlo
APPLICANT: Battistini, Carlo
APPLICANT: Mazue, Guy
APPLICANT: Carlo
APPLICANT: Carlo
APPLICANT: Mazue, Guy
APPLICANT: Carlo
APPLICANT: C
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REGISTRATION NUMBER: 20856
REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 19901129
CLASSIFICATION: AN 186/C1 424
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/443,939
FILING DATE: 30-NOV-1989
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                 CORRESPONDENCE ADDRESS
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CURRENT APPLICATION DATA:
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ADDRESSEE: Fitch, Ev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT ADDRESSEE: P.C. STREET: 1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 YCKNGGFFLRIHPDGRVDGVREKSD 59
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STATE: Illinois
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08187780 Patent No. 5459250
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MEDIUM TYPE: Diskette, 5.25 inch,
MEDIUM TYPE: 360 Kb storage
COMPUTER: IBM or IBM-compatible
OPERATING SYSTEM: PC/MS-POS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/187,780
APPLICATION NUMBER: US/08/187,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: CLAUDIO BASILICO
APPLICANT: DANIELA TALARICO
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ORIGINAL SOURCE:
ORGANISM: Homo
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APPLICATION NUMBER: US
FILING DATE: 19920420
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NAME: Oblon, No. 5288704man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: MANUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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                                                                                                       CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                APPLICATION NUMBER:
FILING DATE: June 2:
APPLICATION NUMBER:
FILING DATE: Decembe
APPLICATION NUMBER:
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STATE: v...
22202
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
                                                                                                                                        FILING DATE: January 25, 1994
                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
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CITY: New York
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805 Third Avenue
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                  December 6, 1991
UMBER: 07/177,506
                                                 UMBER: 07/901,705
June 22, 1992
UMBER: 07/806,771
April 4,
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Pred. No. 0.15;
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 1-145
US-08-187-780-3
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US-08-478-485-3
                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08478485 Patent No. 5883071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: CLAUDIO BASILICO
APPLICANT: DANIELA TALARICO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 753-6237 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 5986/13586-US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07/0 FILING DATE: June 16, 19 ATTORNEY/AGENT INFORMATION: NAME: Howard M. Frankfor
                                                                                                                                                                                 TITLE OF INVENTION: MAMMALIAN GROWTH FACTOR NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby P.C.
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                   COMPUTER READABLE FORM:
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OTHER INFORMATION: Thi
OTHER INFORMATION: COT
OTHER INFORMATION: 910
OTHER INFORMATION: pag
OTHER INFORMATION: app
SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
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STRANDEDNESS: sin
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                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC/MS-DOS
                                                                MEDIUM TYPE: Floppy Diskette, MEDIUM TYPE: 1.44 MB storage
                                                                                                                    ZIP:
                                                                                                                                  COUNTRY:
                                                                                                                                                     STATE:
                                                                                                                                                                     CITY:
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                                                                                                                    10022
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Pred. No. 0.15;
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APPLICATION NUMBER: US/08/478,485

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ADDRESSEE:

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US-08-231-894A-11

; Sequence 11, Application US/08231894A

; Patent No. 5851990

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; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 1-145
US-08-478-485-3
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Best Local Similarity 40.0
Conservative
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TELEFAX: (212) 753-6337
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 145
TYPE:
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FILING DATE: December 6, 1991
APPLICATION NUMBER: 07/17,506
FILING DATE: APPLI 4, 1988
APPLICATION NUMBER: 07/062,925
FILING DATE: June 16, 1987
ATTORNEY/AGENT INFORMATION:
NAME: JOSEPH R. ROBINSON
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 5986/13586-US6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEPHONE: (212) 527-7700
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
                                                                                                                    APPLICANT: FUJISHIMA, AKIRA
APPLICANT: FUKUDA, TSUNEHIKO
TITLE OF INVENTION: BFGF MUTEIN AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 YCKNGGFFLRIHPDGRVDGVREKSD 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
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STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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cy 25, 1994
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Pred. No. 0.15;
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                                                                                                                                 ITS PRODUCTION
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RESULT 11
US-08-231-894A-12
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                                                                                                                                                                                                                                       Sequence 12, Application US/08231894A Patent No. 5851990
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Best Local Similarity 40.0
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: JP 09/000.

APPLICATION NUMBER: JC -APR-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 066381-
APPLICATION NUMBER: J4-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
NAME: RESNICK, DAVID S.
A17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (617) 523-340
TELEFAX: (617) 523-6440
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                         GENERAL INFORMATION:
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FILING DATE: 22-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/873907
                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
ADDRESSEE: & CUSHMAN
                                                                                                                                               APPLICANT: FUJISHIMA, AKIRA
APPLICANT: FUKUDA, TSUNEHIKO
TITLE OF INVENTION: BEGE MUTEIN AND ITS PRODUCTION
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: JP 097655-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 34235
REFERENCE/COCKET NUMBER: 41769-FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
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                            COUNTRY: US
                                                    STATE:
                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
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                                              BOSTON
: MASSACHUSETTS
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                                                                                130 WATER STREET
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Pred. No. 0.15;
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 41:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPULOUS PA
MOLECULE TYPE: PA
HYPOTHETICAL: NO
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,894A
FILING DATE: 22-APR-1994
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LENGTH: 146 amino acid
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FILING DATE: 24-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 0
FILING DATE: 26-APR-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
ADDRESSEE: 6 CUSHMAN
                                                                                                                                                                                                                                                                                    APPLICANT: FUJISHIMA, AKIRA
APPLICANT: FUKUDA, TSUNEHIKO
TITLE OF INVENTION: BEGE MUTEIN AND ITS PRODUCTION
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE:
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                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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COMPUTER: I
                                                                                                                                                               STATE: MASSACHUSETTS COUNTRY: US
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nes 10; Conserv
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                                                                                                                                                   02109
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illarity 40.0%; Pred. No. 0.
Conservative 5; Mismatche
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; ORIGINAL SOURCE: US-08-231-894A-13
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US-08-231-894A-14
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617) 523-644
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 066
APPLICATION NUMBER: JP 066
EILING DATE: 24-MAR-1992
ATTORNEY/AGENT INFORMATION:

NAME: RESNICK, DAVID S.
                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 41 TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: 1
FILING DATE: 24-APR--
                                                                               APPLICATION NUMBER: US/08/231,894A FILING DATE: 22-APR-1994 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
ADDRESSEE: & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NO ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: FUKUDA, TSUNEHIKO
TITLE OF INVENTION: BFGF MUTEIN AND ITS PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                  STREET: STREET: BOSTON
                                              APPLICATION NUMBER: US 07/873907
FILING DATE: 24-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                STATE: MASSACHUSETTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                  130 WATER STREET
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUJISHIMA, AKIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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24-APR-1992
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40.0%; Pred. No. 0.15;
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 JP 097655-1991
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PRIOR APPLICATION DATA:

26-APR-1991

APPLICATION NUMBER: FILING DATE:

JP 066381-1992

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US-08-231-894A-15

Sequence 15, Application US/08231894A

Patent No. 5851990

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-231-894A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/231,894A
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/873907
FILING DATE: 24-APR-1992
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617) 523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEPAX: (617)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO
APPLICATION NUMBER: JP 066381-1992 FILING DATE: 24-MAR-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
ADDRESSEE: 6 CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FUJISHIMA, AKIRA
APPLICANT: FUKUDA, TSUNEHIKO
TITLE OF INVENTION: BEGE MUTEIN AND ITS PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
                                                           PRIOR APPLICATION DATA:
                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 097655-1991
FILING DATE: 26-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sinc
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CITY: BOSTON
STATE: MASSAC
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Local Similarity 40.0%;
nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UZIP: 02109
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; ORIGINAL SOURCE:
US-08-231-894A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 49, Application US/09105678A Patent No. 6103882
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Best Local Similarity 40.0%;
                                                                                                          APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-UN-1998
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION UMBER: JP 172118/1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CON11n, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-6440
                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617) 523-64 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEPAX: (617) 523-6440
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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OPERATING SYSTEM:
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                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                              SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suenaga, Masato
                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moriya, Takeo
Tanaka, Yoko
                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM protein - protein search, using sw model.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq length: 0 seq length: 2000000000
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Match
100.0
100.0
100.0
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67.6
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105
1 PVSVGCFVGFDASE
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11:
12:
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14:
15:
16:
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SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1986.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1987.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1989.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT:*

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SIDSB/gcgdata/geneseq/geneseqp/AA1995.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1996.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*

SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*

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SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT:*
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Gapop 10.0 , Gapext 0.5
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/SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1982.DAT:*
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/SIDSB/gcgdata/geneseq/geneseqp/AA1984.DAT:*
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               AAW53568
AAX17423
AAW53570
AAW53570
AAX17417
AAB98659
AAW57887
AAW57887
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AAW57886
                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (without alignments)
20.060 Million cell updates/sec
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           Cucumber raffinose Cucumber raffinose Cucumber raffinose Cucumber raffinose Soybean raffinose Amino acid sequenc Soybean raffinose Broad bean raffino Amino acid sequenc
                                                                                                                                                                                                                                                      Description
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ALIGNMENTS

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Raffinose synthase gene - useful for preparation of raffinose in transformed plant % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                     07-APR-1998
                                                                                                                                                     JP10084973-A.
                                                                                                                                                                    Cucumis sativus
                                                                                                                                                                                    Cucumber; raffinose synthase; sucrose; galactinol
                                                                                                                                                                                                    Cucumber raffinose synthase residues 61
                                                                                                                                                                                                                    06-JUL-1998 (first entry)
                                                                                                                                                                                                                                     AAW53568;
                                                                                                                                                                                                                                                   AAW53568 standard; peptide;
                       Example 2; Page 17; 26pp; Japanese.
                                                              WPI; 1998-264858/24.
                                                                             (AJIN ) AJINOMOTO KK.
                                                                                             26-JUL-1996;
26-APR-1996;
                                                                                                                     28-APR-1997;
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96JP-0107682
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The present sequence is a cucumber raffinose synthase fragment. Raffinose synthase forms raffinose from sucrose and galactinol, has

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RESULT
AAY17423
ID AAY1
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RESULT
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ID AAW5
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Best Local S
Matches 19
                                                                                                                                     Query Match
Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an optimum pH of 6 to 8 and working temperature of 35 to 40 degrees C, has a molecular weight of 75 to 95 kDa by gel filtration or 90 to 100 kDa by PAGE and SDS-PAGE under reductive conditions and is inhibited by iodoacetamide, N-ethylmaleimide and myoinositol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cucumis sativus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cucumber raffinose synthase peptide SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                        The present invention describes a raffinose synthase, having an activity of forming raffinose from sucrose and galactinol. The raffinose synthase gene can be used for expression in a plant for the production of raffinose. The raffinose synthase can give raffinose from sucrose and galactinol efficiently. The present sequence represents a raffinose contract from sucrose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP11123080-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY17423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY17423 standard; peptide; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Raffinose synthase;
             AAW53570;
                                  AAW53570 standard;
                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                              Example 2; Page 21; 37pp; Japanese.
                                                                                                                                                                                                                                                                                                                 New raffinose synthase gene - for production of raffinose from sucrose and \ensuremath{\mathsf{galactinol}}
                                                                                                                                                                                                                                                                                                                                                                          (AJIN ) AJINOMOTO KK.
                                                                                                                                                                                                                                                                                                                                                                                                24-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                      24-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAY-1999
                                                                                                                                      Local Similarity
les 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        μ
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                                                        w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 100.0%;
1 Similarity 100.0%;
19; Conservative 0
                                                                                                                                                                                                                 peptide from cucumber.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 AA;
                                                                                                                                                                                             19
                                                                                                                                     100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                            ĄĄ,
                                                                                                                                                                                                                                                                                                                                                                                                 97JP-0292969.
                                                                                                                                                                                                                                                                                                                                                                                                                      97JP-0292969.
                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sucrose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                     784
                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            galactinol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 105; DB 19;
Pred. No. 1.5e-10;
; Mismatches 0;
                                                                                                                                                 Score 105;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                                                                                                                                       Mismatches
                                                                                                                                       . 1.5e-10; thes 0;
                                                                                                                                                             DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                             Length 19;
                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
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AAY17417

ID AAY17417

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XX

AC AAY1

AC AAY1

AC Cucu

XX

XX

Cucu

XX

Cucu

XX

FPN JP11

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JP11

XX

PD 11-h

PD 11-h

PD 24-C

XX

XX

PR 24-C

XX

XX

PR (AJI)

PR (AJI)

PR WP11

DR WP11

DR WP11

DR WP11

DR WP11
                                                                                                                                                                                                                                                                                                                                                                                                                                   Ωy
                                                                                                                                                                                                                                                                                               RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP10084973-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cucumis sativus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cucumber; raffinose synthase; sucrose; galactinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cucumber raffinose synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Pages 17-20; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Raffinose synthase gene - useful for preparation of raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAV22250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUL-1996;
26-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                             Cucumis sativus
                                                                                                                                                                                                       Cucumber raffinose synthase
                                                                                                                                                                                                                                                    AAY17417;
                                                                                                                                                                                                                                                                         AAY17417 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        iodoacetamide, N-ethylmaleimide and myoinositol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transformed plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AJIN ) AJINOMOTO KK
                        WPI; 1999-340516/29.
                                                                    24-OCT-1997;
                                                                                          24-OCT-1997;
                                                                                                                11-MAY-1999
                                                                                                                                       JP11123080-A
                                                                                                                                                                                  Raffinose synthase;
                                                                                                                                                                                                                               29-JUL-1999
                                           (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                                                                                                                                               1998-264858/24.
                                                                                                                                                                                                                                                                                                                                                                             l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                     784 AA;
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                                                                                                                                                                                                                               (first entry)
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96JP-0107682.
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                                                                     97JP-0292969
                                                                                          97JP-0292969
                                                                                                                                                                                     sucrose;
                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 105; DB 19;
100.0%; Pred. No. 6.9e-09;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                             784 AA
                                                                                                                                                                                     galactinol.
                                                                                                                                                                                                                                                                                                                                                                                                   Length
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N-PSDB; AAX61238

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RESULT
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Matches 13; Conser
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Best Local S
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                                                                                       The present invention relates to a mutant protein of raffinose synthas in which at least one aromatic amino acid present at the position of about 1-7 amino acids from the N-terminus is deleted or replaced. The mutant protein can be used for reducing the raffinose oligosaccharide content in a plant body. The present protein from soybean, was used in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a raffinose synthase, having an activity of forming raffinose from sucrose and galactinol. The raffinose synthase gene can be used for expression in a plant for the production of raffinose. The raffinose synthase can give raffinose from sucrose and galactinol efficiently. The present sequence represents raffinose synthase from cucumber.
                                                                                                                                                      Disclosure; Page 18-20; 30pp; Japanese.
                                                                                                                                                                      Novel mutant protein of raffinose synthase is useful for reducing raffinose oligosaccharide content in a plant body -
                                                                                                                                                                                                                                              09-JUL-1999;
                                                                                                                                                                                                                                                                03-JUL-2000; 2000JP-0200571.
                                                                                                                                                                                                                                                                                  27-MAR-2001.
                                                                                                                                                                                                                                                                                                    JP2001078783-A.
                                                                                                                                                                                                                                                                                                                      Glycine max.
                                                                                                                                                                                                                                                                                                                                      plant; soybean
                                                                                                                                                                                                                                                                                                                                               Mutant; .mutein;
                                                                                                                                                                                                                                                                                                                                                                 Soybean protein:
                                                                                                                                                                                                                                                                                                                                                                                 17-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                    AAB98659;
                                                                                                                                                                                                                                                                                                                                                                                                                     AAB98659 standard; protein; 780 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New raffinose synthase gene - for production of raffinose from sucrose and galactinol
                                                                        Sequence
                                                                                                                                                                                                           WPI; 2001-313373/33.
                                                                                                                                                                                                                             (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity hes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 pvsvgcfvgfdasepdsrh 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 PVSVGCFVGFDASEPDSRH 19
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VGCFVGFDASEPDSRH 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 25-27; 37pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                784 AA;
                                                                        780 AA;
                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                              99JP-0196036.
                                                                                                                                                                                                                                                                                                                                              raffinose synthase; raffinose oligosaccharide reduction;
                                                                                                                                                                                                                                                                                                                                                                 SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                  67.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Japanese
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                           Score 71; DB Pred. No. 0.00 0; Mismatches
                            0
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Pred. No. 6.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                   DB 22;
0.0025;
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                                            Length 780;
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                            Indels
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AAY30143
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AAW57887
  XXXEXEXEX
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Matches 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
Raffinose synthase;
                                                  Amino acid sequence of a raffinose synthase protein.
                                                                                                  26-OCT-1999
                                                                                                                                                  AAY30143;
                                                                                                                                                                                            AAY30143 standard; Protein; 781 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 31-34; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-324670/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gastrointestinal flora; soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Raffinose synthetase; metabolism modification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soybean raffinose synthetase.
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                                                                                                                                                                                                                                                                                                                   68 vgcfvgfhadeprsrh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 vgcfvgfhadeprsrh 83
                                                                                                                                                                                                                                                                                                                                                                   4 VGCFVGFDASEPDSRH 19
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                                                                                             (first entry)
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plant; sucrose; raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                       67.6%;
81.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 71;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 19;
0.0025;
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AAB49400
IID AAB4
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AC AAB4
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DX Soyb
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Best Local S
Matches 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Page 25-27; 40pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-NOV-1997;
18-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SUMO ) SUMITOMO CHEM CO LTD
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                                             Example 6; Page 24-27; 36pp; English.
                                                                                                     New soybean plant promoters useful for with desired properties
                                                                                                                                                                                                                                                                                                                              30-APR-1999;
01-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-2000; 2000EP-0108962.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant promoter;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB49400 standard;
                                                                                                                                                                 N-PSDB; AAC89523.
                                                                                                                                                                                                                                  Ishige F, Watanabe E,
                                                                                                                                                                                                                                                                                (SUMO ) SUMITOMO CHEM CO LTD
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                                                                                                                                                                                       2001-104537/12.
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                                                                                         desired properties
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13; Conservative
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96JP-0338673.
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                                                                                                                                                                                                                                                                                                                                99JP-0124527.
99JP-0247211.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transgenic plant; desired property.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
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81.2%;
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Pred. No.
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                                                                                                                      generating transgenic
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0.0025;
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RESULT
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                                                                                                      This sequence represents the broad bean raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides in the host organism or cell is changed. Raffinose oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the production of transgenic plants which express genes with desired
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                                                                                                                                                                                                                                                 New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vicia faba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gastrointestinal flora; broad bean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Raffinose synthetase; metabolism modification; food additive;
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                                                                                                                                                                                                                                                                                                                                     0eda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP849359-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Broad bean raffinose synthetase.
                                                                                                                                                                                                                            Claim 1; Page 26-29; 44pp; English.
                                                                                                                                                                                                                                                                                                 N-PSDB; AAV40800
                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                          18-DEC-1997;
                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                          (SUMO ) SUMITOMO CHEM CO LTD
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                                                                                                                                                                                                                                                                                                               1998-324670/29.
  GCFVGFDASEPDSRH 19
                         l Similarity 66.
                                                                                                                                                                                                                                                                                                                                     Wantanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
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                                                                                   799
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                                                                                                                                                                                                                                                                                                                                                                                   96JP-0338673
                                                                                                                                                                                                                                                                                                                                                                                                           97EP-0122417
                                                                                   ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
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81.2%;
                                      60.0%;
66.7%;
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Pred. No. 0.
                                    Score 63; L
Pred. No. 0.
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                                       .052;
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RESULT 1
AAY70978
ID AAY7
XX AAY7
XX O9-A
XX Soyb
XX Soyb
XX Soyb
XX C1on
XX C1on
XX C1on
XX C2oc
PN W020
XX W020
XX W020
XX C1oc
PN U20-C
PF 22-C
XX C1or
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AAY30142
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Best Local 9
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                                                                                                                 Glycine max.
                                                                                                                                      Soybean; raffinose synthase; raffinose sacchar clone sfll.pkl25.d4; nutritional; soy protein.
                                                                                                                                                                       Soybean raffinose synthase from clone sfll.pkl25.d4
                                                                                                                                                                                               09-AUG-2000 (first entry)
                                                                                                                                                                                                                       AAY70978;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 19-21; 40pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAZ10001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-511112/43.
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18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vicia faba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY30142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY30142 standard; Protein; 799 AA.
                                              22-OCT-1999;
                                                                     04-MAY-2000
                                                                                            WO200024915-A2
                                                                                                                                                                                                                                             AAY70978 standard; Protein; 758 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New raffinose synthase gene - is prepared from a plant material
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Raffinose synthase; plant; broad bean; sucrose; raffinose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of a raffinose synthase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-OCT-1999
  (DUPO ) DU PONT DE NEMOURS & CO
                       23-OCT-1998;
                                                                                                                                                                                                                                                                                                     87
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                                                                                                                                                                                                                                                                                                                                                Local Similarity 66. ees 10; Conservative
                                                                                                                                                                                                                                                                                                                          5 GCFVGFDASEPDSRH 19
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|gcfvgfnstepkshh
                                                                                                                                                                                                                                                                                                                                                                                                         799 AA;
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96JP-0338673.
                       98US-0105451
                                             99WO-US24923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97JP-0342899
                                                                                                                                                                                                                                                                                                                                                            60.08;
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                                                                                                                                                                                                                                                                                                                                                            Score 63;
Pred. No.
                                                                                                                                                   raffinose saccharide;
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                                                                                                                                                                                                                                                                                                                                                Mismatches
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0.052;
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RESULT 1
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Best Local (
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                                                                                                              30-APR-1998;
30-APR-1998;
04-DEC-1998;
10-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone sfll.pkl25.d4 isolated from a soybean immature flower cDNA library sfll. Raffinose synthase is involved in the biosynthesis of raffinose and higher homologues in the raffinose saccharide family from sucrose. The present sequence is useful for reducing the raffinose saccharide content of soybean seeds which improves the nutritional quality of the soy protein products derived from them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids and encoded proteins involved in the biosynthesis of raffinose, useful for producing soybean seeds with a reduced raffinose content and therefore improved nutritional quality -
          New sense and antisense genes, useful for altering the level of raffinose in food plants .
                                      WPI; 1999-593144/51.
N-PSDB; AAZ20208.
                                                                      Watanabe
                                                                                                                                                                                        03-NOV-1999
                                                                                                                                                                                                             EP953643-A2
                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                             Beta vulgaris.
                                                                                                                                                                                                                                                                                                                                      Sugarbeet raffinose
                                                                                                                                                                                                                                                                                                                                                           17-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                   AAY32073 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a raffinose synthase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 47-49; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAD00335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Allen
        raffinose
                                                                                                                                                                                                                                                                                                                 Raffinose synthase; sugarbeet; transgenic plant.
                                                                                         (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                   27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 SVGCFVGFDASEPDSRH 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                      Ħ
       in food plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hitz WD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   758 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                      Oeda
                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                             98JP-0120550.
98JP-0120551.
98JP-0345590.
98JP-0351246.
                                                                                                                                                                   99EP-0107430
                                                                                                                                                                                                                                          348
                                                                                                                                                                                                                                                               Location/Qualifiers 227
                                                                                                                                                                                                                               /note-
                                                                                                                                                                                                                                                    note-
                                                                                                                                                                                                                                                                                                                                      synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        70
                                                                                                                                                                                                                                                   "encoded by CCW"
                                                                                                                                                                                                                               "encoded by CCR"
                                                                                                                                                                                                                                                                                                                                                                                                    783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 62; DB
Pred. No. 0.07
3; Mismatches
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0.071;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            haming leaf cDNA by PCR. Probes or primers generated from plant raffinose synthase genes (see AAZ20207-10) may be used to obtain other raffinose synthase genes by labeled detection or amplification (claimed). These genes may be used to control the levels of raffinose produced in plants. Antisense genes can be used to knock out existing gene activity, and sense genes to increase the level of gene activity. The resulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacteria, providing general health advantages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents sugarbeet raffinose synthase, a protein that can bind a D-galactosyl group through an alpha(1-6) bond to the hydroxy group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. cDNA (see AAZ20208) encoding the enzyme was isolated from sugarbeet cv. haming leaf cDNA by PCR. Probes or primers generated from plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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                                                                            Nucleic acids and encoded proteins involved in the biosynthesis of raffinose, useful for producing soybean seeds with a reduced raffinose content and therefore improved nutritional quality -
                               Claim 2;
                                                                                                                                                                                                                                                                             Allen SM, Hitz WD;
                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                            22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY70976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY70976 standard; Protein; 770 AA.
                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
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                                                                                                                                                                                           2000-350754/30.
DB; AAD00333.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             raffinose synthase; raffinose saccharide; soybean; rls24.pk0017.g10; nutritional; soy protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sativa.
                               Page 40-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 22-24; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     783 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthase from clone rls24.pk0017.g10
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represented as base pairs 693-797 i
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73.3%;
                            58pp; English.
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Pred. No.
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0.11;
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RESULT 14
AAG16865
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  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a raffinose synthase from clone ris24.pk0017.g10 isolated from a rice infected leaf cDNA library rls24. Raffinose synthase is involved in the biosynthesis of raffinose and higher homologues in the raffinose saccharide family from sucrose. The present sequence is useful for reducing the raffinose saccharide content of soybean seeds which improves the nutritional quality of the soy protein products derived from them.
14-MAY-1999;
14-MAY-1999;
18-MAY-1999;
19-MAY-1999;
20-MAY-1999;
21-MAY-1999;
                                                                                                                                                                                                                                                                           09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 17671.
                                                                                                06-MAY-1999;
07-MAY-1999;
                                                                                                                      05-MAY-1999;
06-MAY-1999;
                                                                                                                                           30-APR-1999;
04-MAY-1999;
                                                                                                                                                                          23-APR-1999;
28-APR-1999;
                                                                                                                                                                                                                                                      01-APR-1999;
06-APR-1999;
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05-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                          termination
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-OCT-2000
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                                                                                                                                                                  30-APR-1999;
                                                                                                                                                                                                 21-APR-1999;
23-APR-1999;
                                                                                                                                                                                                                       16-APR-1999;
19-APR-1999;
                                                                                                                                                                                                                                             08-APR-1999;
                                                                                                                                                                                                                                                                                                                                                       25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                             06-SEP-2000
                                                                 14-MAY-1999;
14-MAY-1999;
                                                                                        11-may-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               770 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                       2000EP-0301439
          990S-0128714

990S-0129845

990S-0130449

990S-0130891

990S-0131449

990S-0132048

990S-0132484

990S-0132485

990S-0132485

990S-0132486

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990S-013427

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99US-0126785.
99US-0127462.
99US-0128234.
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99US-0123180.
                                                                                                                                                                                                                                                                                                 99US-0123548.
99US-0125788.
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57.9%;
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Pred. No. 17;
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promoter;
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27-JUL- 28-JUL- 02-AUG- 02-AUG-	7-JUL-	3-JUL-	3-JUL-	2-301-	יייטני-	1-501-	0-JUL-	0-JUL-	9-JUL-	9-JUL-	19-JUL-	16-JUL-	15-JUL-	13-JUL- 14-JUL-	2-JUL-	9-JUL-	2-JUL- 6-JUL-	1-306-	30-JUN-	B-JUN-	3-JUN-	2-JUN- 3-JUN-	1-JUN- 1-JUN-	8-JUN-	18-JUN-	18-JUN-	18-JUN-	18-JUN-	18-JUN-	18-JUN-	-JUN-	-JUN-	-JUN-	B-JUN-	-JUN-	3-JUN-	1-JUN-	-MAY	4-MAY-
1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	, 666 1666	1999;	1999;	;6661	1999;	1999;	, 6661 1686	1999;	1999;	1999;	,6661	1999;	1999;	1999;	1999;	; 6661 :	1999;	1999;	1999;	;6661 ;6661	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	1999;	999;
990S-014 990S-014 990S-014 990S-014	908-01 908-01	90S-01	905-01 905-01	90S-01	908-01	9US-01	90S-01	908-01	908-01	905-01	90S-01	908-01	905-01	90S-01 90S-01	908-01	9US-01	90S-01 90S-01	908-01	9US-01	9US-01	908-01	90S-01	90S-01 90S-01	905-01	90S-01	9US-01	908-01	908-01	9US-01	908-01	908-01	90S-01	908-01	9US-01	905-01	905-01	9US-01 9US-01	905-01	905-01
145919. 145951. 146386.	5913. 5918.	5218. 5224.	5192.	5085.	5088.	4814.	4632.	4352.	4334	4332.	4325. 4331.	4086.	4005.	3542. 3624.	2977.	2803.	2055. 2390.	2154.	1287.	0823.	0354.	9899. 0353.	9763.	9750.	9462.	9460.	9458.	9457.	9455.	9454.	9453.	9119. 9452.	8847.	8094	7724.	7528.	6782. 7222.	6392.	5629.
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28-OCT-1999;
29-OCT-1999;
25 FEB-1999
05-MAR-1999
09-MAR-1999
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25-MAR-1999
26-AR-1999
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RR 17 - MUC - 1999 99US - 014864.

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Search completed: November 30, 2001, 09:42:57 Job time: 156 sec

GenCore version Copyright (c) 1993 - 2000

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ALIGNMENTS

RESULT B86320

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3-phosphoserine phosphatase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: B86320
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A.;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A. Accession: B86320
                                                                                                            phosphoserine phosphatase (EC 3.1.3.3) precursor, chloroplast [validated] - Arabidop N;Alternate names: 3-phosphoserine phosphatase C;Speciaes: Arabidopsis thaliana (mouse-ear cress) C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000 C;Accession: T51362 R;Ho, C:; Noji, M.; Saito, K. J. Biol. Chem. 274, 11007-11012, 1999 A;Title: Plastidic pathway of serine biosynthesis. Molecular cloning and expression A;Reference number: Z25385 A;Accession: T51362
                            A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-295 <HOC>
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A;Molecule type: DNA
A;Residues: 1-295 <STO>
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A; Cross-references: EMBL: AB018408; PIDN: BAA33806.1
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64.3%;
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C;Species: Agaricus bisporus (cultivated mushroom)
C;Date: 06-Dec-1996 #sequence_revision 07-Feb-1997 #text_change 21-Jul-2000
C;Accession: $68584; $68586; $58342
R;de Groot, P.W.J.; Schaap, P.J.; Sonnenberg, A.S.M.; Visser, J.; van Griensven, L.J.L.I.J.Mol. Biol. 257, 1008-1018, 1996
A;Title: The Agaricus bisporus hypa gene encodes a hydrophobin and specifically accumula A;Reference number: $68584; MUID:96192085
A;Accession: $68584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X90818; NID:g1235753; PIDN:CAA62331.1; PID:g1235754
A;Accession: 568586
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: EMBL:X89242; NID:g944820; PID:g944821
A;Cross-references: EMBL:X89242; NID:g944820; PID:g944821
C;Genetics:
A;Gene: hypa
A;Introns: 18/3; 40/1; 96/3
C;Superfamily: 1G2 protein
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A; Map position: 1
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                                                                                                                                                                            hypothetical protein L518_F3_81 - Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: Mycobacterium leprae C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #tex C;Accession: S73023 R;Smith, D.R.; Robison, K. submitted to the EMBL Data Library, November 1993 submitted to the EMBL Data Library, November 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: nucleic acid sequence not shown
                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-301 <SMI>
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A; Residues: 1-112 <DEG>
A;Cross-references: EMBL:000023; NID:9467194; PIDN:AAA17366.1; PID:9467209 C;Superfamily: Mycobacterium leprae hypothetical protein L518_F3_81
                                                                                                                                     A; Description: Mycobacterium A; Reference number: S72591
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                                                                                                                                                                                                                                                                                                                                                                                                               PINLGAFLGFDCT 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.9%;
46.2%;
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                                                                                                                                                              leprae
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Pred. No. 4.3;
5; Mismatches
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                                                                                                                                                                 November 1993 cosmid L518.
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                                                                                                                                                                                                                                                         25-Apr-1997 #text_change 23-Mar-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Query Match

41.98;

Score 44;

DВ

2

Length 301

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terminus protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: FlyBase:FBgn0003683
C;Superfamily: Drosophila terminus protein
C;Keywords: DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:M19140; NID:g158535; PID:g158536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-428 <BAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A43741; A; Accession: A43741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Transcripts of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Baldarelli, R.M.; Mahoney, P.A.; Salas, F.; Gustavson, E.; Boyer, P.D.; Chang, Dev. Biol. 125, 85-95, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: A43741
                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T22P11.70 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 19-May-2000 C;Accession: T48269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: FlyBase:term
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Best Local Similarity
7; Conserve
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A;Note: T22P11.70
C;Superfamily: Arabidopsis thaliana hypothetical protein F13M22.7
                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: Z24490
A; Accession: T48269
                                                                                                                                                                                                                                                                                                                                                                                                                         R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, submitted to the Protein Sequence Database, 1
                                   RESULT
JC1450
                                                                                                                                                                                                                                                                                                          A; Experimental source: cultivar Columbia; BAC
                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL: AL162971
                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-498 <BEV>
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fibroblast growth factor receptor 4 - N; Contains: protein-tyrosine kinase (
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Matches 7
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Matches 8; Conser
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                                                                                                  GCFTGFDKSD 141
                                                                                                                               GCFVGFDASE 14
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50.0%;
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70.0%;
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Pred. No.
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Pred. No.
      OEC
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Mismatches
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17;
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                                                                                                                                                                                                     DΒ
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A; Description: receptor mediating effects of fibroblast growth factor
A; Note: expressed in normal lung; expressed in some carcinomas
C; Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
C; Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor;
F;11-72/Domain: immunoglobulin homology <IM2>
F;218-238/Domain: immunoglobulin homology <IM2>
F;218-238/Domain: immunoglobulin homology <IM2>
F;239-650/Domain: intracellular *status predicted <IMT>
F;331-398/Domain: protein kinase homology <KINN>
F;331-399/Domain: protein kinase ATP-binding motif
F;310-1329/Region: protein kinase ATP-binding motif
F;104,136,157,168/Binding site: carbohydrate (Asn) (covalent) *status predicted
F;465,478/Binding site: magnesium (Asn, Asp) *status predicted
F;465,478/Binding site: magnesium (Asn, Asp) *status predicted
F;491/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene 120, 291-295, 1992
A;Title: Cloning, expression and tissue distribution of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M91599; NID:g204137; PIDN:AAA41157.1; PID:g204138 R;Lai, C.; Lemke, G. Neuron 6, 691-704, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                     R;Miller, N.; Kramer, J.; Smith, A. submitted to the EMBL Data Library, May 1998 A;Description: The sequence of C. elegans co.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F22F7.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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                                                                                                                                   A; Introns: 18/2;
                                                                                                                                                                                      A; Gene: CESP: F22F7.6
                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-313 <MIL>
A;Residues: 1-313 <MIL>
A;Cross-references: EMBL:AF067937; PIDN:AAC19217.1; GSPDB:GN00023; CESP:F22F7.6
A;Experimental source: strain Bristol N2; clone F22F7
                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 465-518 <LAI>
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A; Residues: 1-650 <HOR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Gene: FGFR4; tyro-9
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                             Local
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291-295, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
9; Conserv
     Similarity
7; Conserv
                                                                                                                                82/3; 117/1; 210/2; 241/3;
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                          41.08;
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                          Score 43;
Pred. No.
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Pred. No. 26;
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                             DB 2;
18;
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hypothetical protein [imported] - Arabidopsis thaliana
()Species: Arabidopsis thaliana (mouse-ear cress)
C)Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: F86185
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors; Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, Y.H.; Lil, Y.; Liu, S.X.; Liu, S.X.; Liu, S.X.; Liuos, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference number: A86141; MUID:21016719
A;Accession: F86185
                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosidues: 1-447 <ROUY
A;Cross:references: EMBL:ACO04681; NID:g3298532; PID:g3298536
A;Cross:references: EMBL:ACO04681; NID:g3298532; PID:g3298536
A;Experimental source: cultivar Columbia
A;Experimental source: cultivar Columbia
A;Experimental source: Cultivar Columbia
M; Cross: Found File Columbia
M; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
M; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
M; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
M: Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
M: Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
M: Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
M: Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
M: Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
M: Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
M: Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
M: Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
M: Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
M: Koo, H.; Moffat, M.; Moffat, M.; VanAken, S.E.; Umayam, L.; Tallon,
M: Koo, H.; Moffat, M.; Moffat, M.; VanAken, S.E.; Umayam, L.; Tallon,
M: Koo, H.; Moffat, M.; Moffat, M.; VanAken, S.E.; Umayam, L.; Tallon,
M: Koo, H.; Moffat, M.; Moffat, M.; VanAken, M.; VanAken, S.E.; Umayam, L.; Tallon,
M: Koo, H.; Moffat, M.; Moffat, M.; VanAken, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Description: Arabidopsis thaliana chromosome II BAC T26B15 genomic sequence A;Reference number: 214678
A;Accession: T02547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein At2g32480 [imported] - Arabidopsis thallana N;Alternate names: hypothetical protein T26B15.4 C;Species: Arabidopsis thallana (mouse-ear cress) C;Date: 05-Mar 1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Thehes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A84420; A; Accession: F84733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; submitted to the EMBL Data Library, July 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: T02547; F84733
R;Rounsley, S.D.; Kaul, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 1
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A; Residues: 1-441 <STO>
A; Cross-references: GB:
                                                 A; Map position:
                                                                                                                                                                                                A; Cross-references:
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                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
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                                                                                             T26B15.4; At2g32480
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Escherichia coli probable zinc proteinase yael
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                                                                                                                                                                                           GB:AE002093;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152
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57.1%;
                                                                                                                                                                                           NID: g3298536;
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                                                                                                                                                                                           PIDN:AAC25930.1; GSPDB:GN00139
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Biochim. Biophys. Acta 1252, 185-188, 1995
A;Title: Amino-acid sequence of rat liver kynureninase.
A;Reference number: S59898; MUID:96049498
A;Status.
                                                                                                                                                                                                                                                                        R;Toma, S.; Nakamura, M.; Tone, S.; Okuno, E.; Kido, R.; Breton, J.; Avanzi, FEBS Lett. 408, 5-10, 1997
A;Title: Cloning and recombinant expression of rat and human kynureninase. A;Ritle: Cloning and recombinant expression of rat and human kynureninase. A;Reference number: Z24527; MUID:97324088
A;Accession: T48675
A;Cossion: T48675
A;Cossion: T48675
A;Coss-references: EMBL:U68168; NID:91532215; PIDN:AAC53206.1; PID:91532216
A;Experimental source: liver
C;Function:
A;Experimental source: liver
C;Function: EC 3.7.1.3 [validated; MUID:97324088]
A;Pathway: biosynthesis of NAD cofactors
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kynureninase (EC 3.7.1.3) [validated] - rat
N;Alternate names: L-kynurenine hydrolase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 21-Jul-2000
C;Accession: T48675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
hypothetical protein C15H9.7 - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 20-Sep-1999 #sequence revision ?^---- ?^^~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jul-1996 #sequence_revision 13
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                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Keywords: hydrolase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
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Best Local Similarity
Matches 7; Conserv
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Best Local S
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                                                                                                                         244
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                                                                                                                         GCFVGFD 250
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8; Conserv
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57.1%;
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                                                                                                                                                                                             0;
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Pred. No.
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Pred. No.
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     20-Sep-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                             DB
27;
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27
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A; Introns: 30/3; 70/1;
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       hypothetical protein b1 - loblolly pine
C;Species: Pinus taeda (loblolly pine)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: CESP:C15H9.7
                                                           T46623
                                                                                                                              В
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                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-546 <KUN>
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Matches
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Best Local
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                                                                                                                                                  2 VSVGCFVGFDASE-PD 16
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                                                                                                                              VSALCFIGFLAAEAPD
                                                                                                                                                                                                  10;
                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                     Bacillus subtilis
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                    40.5%;
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Score 42.5; Pred. No. 39;

DB

Length 546;

Indels

1.

Gaps

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R; Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber R; Kunst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Carter, N.M.; C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galizzi, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Interpretation, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino, Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino, Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino, A.; Mathors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete y. M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanli Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanli R.; Winters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipat, A.; Yamanoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A.; Aluthors: Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A.; Reference number: A69580; MUID:98044033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein yndJ - Bacillus subtilis C;Species: Bacillus subtilis C;Date: 05-Dec-1997 #sequence_revision 05-Dec-C;Accession: A69890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:U56965; NID:g1945492; PID:g1293837; PIDN:AAB52668.1; GSPDB:GA;Experimental source: strain Bristol N2; clone C15H9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-478 <BEN>
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submitted to the EMBL Data Library, April 1996
A; Description: The sequence of C. elegans cosmid C15H9.
A; Reference number: Z18364
A; Accession: T15516
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                                                                                                                                                                                                                                                                                  A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                       A;Cross-references: GB:Z99113; GB:AL009126; A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                  strain
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s; Pred. No. 28;
0; Mismatches
hypothetical protein
                                                                                                                                                        NID:g2634090; PIDN:CAB13664.1; PID:g26341
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C:Accession: 146623 : Eunkhouser, E.A.; Mewton, R.J.; Cairney, J. submitted to the EMBL Data Library, July 1995 A:Description: Cloning of a chitinase homolog which lacks chitin binding sites and is do right of the EMBL Data Library, July 1995 A:Decession: 14662; translated from Ge/EMBL/DDBJ A. Medicule type: mBay translated from Ge/EMBL/DDBJ A. Micross-references: EMBL/U31109; MID:9974285; PID:9974288 A. Experimental source: strain s6PT2xs6FT3; 8 month seedlings A. Experimental source: strain s6PT2xs6FT3; 8 month seedlings A. Experimental source: strain s6PT2xs6FT3; 8 month seedlings G. S. Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Length 72; Best Loss Inlantity 63.6; Prod Ab. 59; Loss Inlantity 64.6; Best Loss Inlantity 64.6; Be
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            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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       KYNU_CAEEL
GL19_ARATH
HTS1_COCCA
VE7_HPV32
POR1_BOVIN
POR1_BOVIN
POR1_BOVIN
POR1_BOVIN
AMD_CHICAN
ALBU_CHICAN
ALBU_CHICAN
ALBU_CHICAN
ALBU_CHICAN
AMO_TICAN
DPO1_THETH
DSC1_BOVIN
E2B1_METJA
VGLG_HSVE4
MCAT_HOMAE
MCAT_HOMSE
MRAL_SACSU
KR1_TYCR
AMO_ECOLI
RRPO_ROTBU
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6 caenorhabdi
6 caenorhabdi
6 cochliobolu
7 human papil
9 bos taurus
5 oryctolagus
2 mus musculu
4 saccharomyc
9 trypanosoma
escherichia
Bovine rota
5 bovine rota
9 porcine rot
8 simian 11 r
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homo sapien
gallus gall
pichia angu
klebsiella
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RESULT 2
TERM_DROME
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RA Addams D.), Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Andams M.D., Celniker S.E., Lih P.W., Hoskins R.A., Galle R.F., Ra Amanatides P.G., Scherer S.E., Hilb P.W., Hoskins R.A., Galle R.F., Ra Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N., Ra George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N., Ra George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N., Ra George R.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Ra Hardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D., Ra Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D., Ra Barlow R.M., Baxer E.G., Hell G., Nelson C.R., Miklos G.L.G., Ra Barlow R.M., Baxer E.G., Hell G., Nelson C.R., Miklos G.L.G., Ra Barlow R.M., Baxer E.G., Hell G., Nelson C.R., Miklos G.L.G., Ra Barlow R.M., Baxer E.G., Hell G., Nelson C.R., Miklos G.L.G., Ra Berson K.Y., Beans P.V., Berman B.P., Bhandari D., Bolshakov S., Ra Burtis K.C., Busam D.A., Butler H., Gargenct L.B., Drottier P., Bensley E.M., Ra Berson K.D., Devley S., Dahke C., Davenport L.B., Davies P., Ra Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Ra Holl R.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Ra Hoslin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., Ra Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Kan Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., Ra Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., Ra Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Ra Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Ra Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Ra Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Ra Ra Bart K., Ramington K., Sanders R.D.C., Scheeler F., Sprad In., Ketchum K., Sunger E., Sprad In., Ketchum K., Strong R., Sun E., Yen S., Yeh R., F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Yeh R., F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baldarelli R.M., Mahoney P.A., Salas F., Gustavson E., Bo
Chang M.-F., Roark M., Lengyel J.A.;
"Transcripts of the Drosophila blastoderm-specific locus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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01-0CT-1989 (Rel. 12, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
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[2]
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Pred. No.
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SO FIRM DRR FRA DRR FR
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                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-96049498; PubMed-7578221;
Takeuchi F., Tsubouchi R., Yoshino M., Shibata Y.;
"Amino-acid sequence of rat liver kynureninase.";
Biochim. Biophys. Acta 1252:185-188(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KYNU_RAT STANDARD; PRT; 404 AA.
P70712; Q9QW90;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
kYNURENINASE (EC 3.7.1.3) (L-KYNURENINE HYDROLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M19140; AAA28928.1; ... EMBL; AE003520; AAF49257.1; ...
                                                               TISSUE=Liver, and Kidney;
MEDLINE=96314506; PubMed=8706755;
Alberati-Giani D., Buchli R., Malherbe
Koehler C., Lahm H.-W., Cesura A.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR;
                                                                                                                                                                                                                                                                    Toma S., Nakamura
Avanzi N., Cozzi I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0003683; term
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-WISTAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KYNU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZN_FING
kynureninase.
Eur. J. Bioch
                                                "Isolation and expression
                                                                                                                                                                         SEQUENCE OF 19-117 FROM N.A.,
                                                                                                                                                                                                                                                                                                                    MEDLINE-97324088; PubMed-9180257
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                "Cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; IPR000822; Znf-C2H2.
pS50157; ZINC_FINGER_C2H2_2; UNKNOWN_1.
ps550157; Zinc-finger; Developmental protein.
ing; Zinc-finger; Developmental protein.
325 346 C3H-TYPE.
     Biochem
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144
428 AA;
                                                                                                                                                                                                                                                akamura M., Tone S., Okuno E., Kido R., Breton J.,
Cozzi L., Speciale C., Mostardini M., Gatti S., Benatti
nd recombinant expression of rat and human kynureninase
                                                                                                                                                                                                                       408:5-10(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Liver;
       239:460-468(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19
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                                                                                                                                                                                                                                                                                                                                                                       AND PARTIAL SEQUENCE.
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                                                     of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2:
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Þ
                                                       Ŋ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                              AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F545653F738AE434
                                                       CDNA
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                                                          clone
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                                                                                                  Ρ.
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7.7;
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                                                                                                     Broger C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murinae; Rattus.
                                                                                                          Lang
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                                                                                                          G.,
                                                                                                                                                                                                                                                                              Benatti L.;
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Query Match
Best Local (
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                                                                                                                                                                                                                                               KYNU_CAEEL STAN
Q18026;
15-DEC-1998 (Rel. 3
15-DEC-1998 (Rel. 3
15-DEC-1998 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase; | MOD_RES
                                                                                                                                                                                                                                                                                                                            CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                  Bentley D.;
Submitted (MAY-1996) to
-1- CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                 STRAIN-BRISTOL N2;
                                                                                                                                                                          Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                       Caenorhabditis elegans.
                                                                                                                                                                                                                        C15H9.7
                                                                                                                                                                                                                                    PROBABLE KYNURENINASE
                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U68168; AAC53206.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                      244
                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 7; Conserv
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                     COFACTOR: PYRIDOXAL PHOSPHATE (BY COFACTOR: PYRIDOXAL PHOSPHATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: HOMODIMER,
SUBCELLULAR LOCATION: CYTOPLASMIC
TISSUE SPECIFICITY: HIGH LEVELS II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: L-3-HYDROXYKYNURENINE + H(2)O = 3-
HYDROXYANTHRANILATE + L-ALANINE.
COFACTOR: PYRIDOXAL PHOSPHATE.
CATALYME REGULATION: INHIBITED BY O-METHYLBENZOYLALANINE (OMBA).
PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF NAD COFACTORS FROM
SUBCELLULAR LOCATION: C
SIMILARITY: BELONGS TO
TO CLASS-V OF PYRIDOXAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: HIGH LEVELS IN LIVER AND KIDNEY. ALSO DETECTED IN HEART, RETINA, OVARY. LUNG, TESTIS AND BRAIN. INDUCTION: INHIBITED BY THIOL REAGENTS AND HEAVY METAL IONS. SIMILARITY: BELONGS TO THE KYNURENINASE FAMILY. SLIGHTLY RELATED
                                                                                                                                                                                                                                                                                                                                                                                   GCFVGFD 11
||||||
| GCFVGFD 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRYPTOPHAN THROUGH THE KYNURENINE PATHWAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BETA-LYASE ACTIVITY: L-KYNURENINE + H(2)O - ANTHRANILATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYDROXYANTHRANILIC ACIDS (3-OHAA), RESPECTIVELY. HAS A PREFERENCE FOR THE L-3-HYDROXY FORM. OPTIMUM ACTIVITY IS AROUND PH 9.0 FOR L KYN AND AROUND 8.5 FOR L-3OHKYN. ALSO HAS CYSTEINE-CONJUGATE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: CATALYZES THE CLEAVAGE OF L-KYNURENINE (L-KYN) AND L-3-HYDROXYKYNURENINE (L-3OHKYN) INTO ANTHRANILIC (AA) AND 3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pyridoxal phosphate; Acetylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276
18
26
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                           37, Created)
37, Last sequence update)
37, Last annotation update)
NASE (EC 3.7.1.3) (L-KYNURENINE HYDROLASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      276
18
7
26
118
118
7
                                                                                                                                                                            Nematoda; Chromadorea; cinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               41.0%;
                                                                      the EMBL/GenBank/DDBJ
L-KYNURENINE + H(2)0 •
                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYRIDOXAL PHOSPHATE.
A -> T (IN REF. 1).
D -> N (IN REF. 1).
T -> S (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACETYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A -> T (IN REF. 1).
D -> N (IN REF. 1).
T -> S (IN REF. 1).
FF1CC95E3202ECEC C
            PLASMIC (BY SIMILARITY).

KYNURENINASE FAMILY. SLIGHTLY RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                              478
                                           SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                         Rhabditida; Rhabditoidea;
                                                                         •
                                                                        databases.
- ANTHRANILATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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RESULT
GL19_AF
RX MEDLINE-21016721; PubMed-11130714;
RX MEDLINE-21016721; PubMed-11130714;
RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Wada T.,
RA Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S.,
RA Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T.,
RA Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T.,
RA Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T.,
RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Huang E., Spiegel L., Gordes M., Courtney M., Dante M.,
RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strowmatt C.,
RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strowmatt C.,
RA Wagner M.Cherson C., Wollam A., Yoakum M., Bell M., Dedhia N.,
RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,
RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,
RA Martienssen R., McCombbe W.R., Willson R.K., Murphy G., Bancroft I.,
RA Martienssen R., McCullagh B., Robben J., Grymonprez B., Zimmermann W.,
RA Ramsperger U., Wedler H., Balke K., Wedler E., Peters S.,
RA Weitzenegger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S.,
RA Peldpausch M., Lamberth S., Villarroel R., Gielen J., Ardiles W.,
RA Peldpausch M., Lamberth S., Villarroel R., Gielen J., Ardiles W.,
Ra Pentson T., Medeler H., Balke K., Wedler K., Rudd S., Schoof H.,
Ra Pentson M., Lamberth S., Villarroel R., Bentson M., Fransz P.F.;
RA Pentson M., Lamberth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
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Best Local S
Matches 7
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1 20-AUG-2001 (Rel. 40, Created)

1 20-AUG-2001 (Rel. 40, Last sequence update)

2 20-AUG-2001 (Rel. 40, Last sequence update)

2 20-AUG-2001 (Rel. 40, Last annotation update)

2 3 ATABITY GERMIN-LIKE PROTEIN SUBFAMILY 1 MEMBER 9 PRECUF

3 ATABITY OF A STATE OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WormPep; C15H9.7; CEU
Hypothetical protein;
BINDING 289 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GL19_ARATH
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                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3702;
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289 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
54049 MW; E889450929E094BD CRC64;
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structural analysis of Arabidopsis thaliana c
Sequence features of the regions of 1,456,315
physically assigned P1 and TAC clones.";
DNA Res. 5:41-54(1998).
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METAL
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Scott-Craig J.S., Panaccione D.G., Pocard J.-A., Walton J.D.; Scott-Craig J.S., Panaccione D.G., Pocard J.-A., Walton J.D.; The cyclic peptide synthetase catalyzing HC-toxin production filamentous fungus Cochliobolus carbonum is encoded by a 15.7-kilobase open reading frame ", J. Biol. Chem. 267:26044-26049(1992).

-i- FUNCTION: THIS PROTEIN IS A MULTIFUNCTIONAL ENZYME, ABLE
                                                                                                                                                 Cochliobolus carbonum (Bipolaris zeicola).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Pleosporales; Pleosporaceae; Cochliobolus.
                                                                                           STRAIN-SB111;
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                                                                              MEDLINE=93100328; PubMed=1281482;
                                                                                                            SEQUENCE FROM N.A.,
                                                                                                                                    NCBI_TaxID=5017;
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FUNCTION: MAY PARY A ROLE IN PLANT DEFENSE. HAS PROBABLY NO FUNCTION: MAY PARY A ROLE IN PLANT DEFENSE. HAS PROBABLY NO CONALATE OXIDABE ACTIVITY EVEN IF THE ACTIVE SITE IS CONSERVED. SUBUNIT: OLIGOMER (BELIEVED TO BE A PENTAMER BUT PROBABLY HEXAMER) (BY SIMILARITY).
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55.6%;
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Pred. No. 10;
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E7 PROTEIN.
E7.
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pfam; pF00668; Condensation; !
pfam; PF00550; pp-binding; 4.
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InterPro;
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                     Papillomavirus.
NCBI_TaxID=10612;
                                            Viruses; dsDNA viruses,
                                                     Human papillomavirus
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nes 8; Conserv
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                                                                                                                                                                                                                       5 GCFVGFDASEPDSR 18
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ACYL CARRIER (ACP) 2.
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PHOSPHOPANTETHEINE (BY SIMILARITY).
7 MW; 0331D9C5400163A5 CRC64;
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Pfam; PF00527; E7; 1.
Early protein; Transcription regulation; Tr
DNA-binding; Trans-acting factor.
DOMAIN
97 100 C-XX-C MOTIF 1
DOMAIN 97 100 C-XX-C MOTIF 2
SEQUENCE 104 AA; 11591 MW; F9DFCBC0B6D8
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Curr Top. Microbiol. Immunol. 186:13-31(1994).
-1- FUNCTION: E7 PROTEIN HAS BOTH TRANSFORMING AND TRANS-J
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P45879;
01-NOV-1995
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                                                                                                                                CONSTITUTES A large-conductance anion channel in astrocytic plasma membranes.";

Proc. Natl. Acad. Sci. U.S.A. 91:499-503(1994).

SMALL HYDROPHILIC MOLECULES; IT ADDETS AN OPEN CONFORMATION AT LOW SMALL HYDROPHILIC MOLECULES; IT ADDETS AN OPEN CONFORMATION AT POTENTIALS OR ZERO MEMBRANE POTENTIAL AND A CLOSED CONFORMATION AT POTENTIALS ABOVE 30-40 MV. THE OPEN STATE HAS A WEAK ANION SELECTIVITY ABOVE 30-40 MV. THE OPEN STATE HAS A WEAK ANION SELECTIVES.

WHEREAS THE CLOSED STATE IS CATION-SELECTIVE.
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Mammalia; Eutheria;
Bovidae; Bovinae; Bo
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 1 (VDAC-1)
(PLASMALEMMAL PORIN) (BRAIN-DERIVED VOLTAGE-DEPENDENT ANION CHANNEL 1)
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Kremer M., Deutzmann R., Th
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Buettner R., HOLEL
Buettner R., Fishman
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prINTS; pR00185; EUKARYTPORIN.
pROSITE; pS00558; EUKARYOTIC_PORIN;
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 1 (VDAC-1) (OUTER
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Eukaryota; Metazoa; Chordata; Craniata; Vei
Mammalia; Eutheria; Lagomorpha; Leporidae;
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                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                     EMBL; AF209725; AAF22835.1; -.
                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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WHEREAS THE CLOSED STATE IS CATION-SELECTIVE (BY SIMILARITY).

WHEREAS THE CLOSED STATE IS CATION-SELECTIVE (BY SIMILARITY).

MEMBRANE (BY SIMILARITY).

DOMAIN: CONSISTS MAINLY OF MEMBRANE-SPANNING SIDED BETA-SHEETS.

DOMAIN: CONSISTS MAINLY OF MEMBRANE-SPANNING SIDED BETA-SHEETS.

SIMILARITY: BELONGS TO THE EUKARYOTIC MITOCHONDRIAL PORIN FAMILY.
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; 2E6BB2055FCD7849 CRC64;
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23;
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InterPro; IPR001925; Euk_porin. pfam; PF01459; Euk_porin; 1. PRINTS; PR00185; EUKARYTPORIN.

PROSITE; PRINTS; PR00185;

PS00558; EUKARYOTIC_PORIN;

Porin; Mitochondrion; Acetylation

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                                                                                                                                                                                                                                                                                                                                                                                   RY CHARACTERIZATION, AND ALTERNATIVE SPLICING.

RX MEDLINE-20202612; PubMed-10716730;

RX MEDLINE-20202612; PubMed-10716730;

RA Buettner R., Papoutsoglou G., Scemes E., Spray D.C., Dermietzel R.;

RA Buettner R., Papoutsoglou G., Scemes E., Spray D.C., Dermietzel R.;

RT anion channel isoform.

RT anion channel isoform.

RI PIOC. Natl. Acad. Sci. U.S.A. 97:3201-3206(2000).

RL OC. -1- FUNCTION. FORMS A CHANNEL THE CHANNEL ALLOWS DIFFUSION OF COMPORMATION AT LOW SMALL HYDROPHILIC MOLECULES; IT ADOPTS AN OPEN COMPORMATION AT LOW SMALL HYDROPHILIC MOLECULES; IT ADOPTS AN OPEN COMPORMATION AT LOW SMALL HYDROPHILIC MOLECULES; IT ADOPTS AN OPEN COMPORMATION AT POTENTIALS OR ZERO MEMBRANE POTENTIAL AND A CLOSED CONFORMATION AT POTENTIALS ABOVE 30-40 MV. THE OPEN STATE HAS A WEAK ANTON SELECTIVITY

C ABOVE 30-40 MV. THE OPEN STATE HAS A WEAK ANTON SELECTIVITY

C HERBRANE OF MITOCHONDRIA AND PLASMALEMMAL VDACI (PL-VDACI) IN OUTER MEMBRANE OF MITOCHONDRIA AND PLASMALEMMAL VDACI (PL-VDACI) IN
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MOD_RES
BINDING
SEQUENCE
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 1 (VDAC-1) (MVDAC1)
(MVDAC5) (OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN 1) (PLASMALEMMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sampson M.J., Lovell R.S., Craigen W.J.; "Isolation, characterization, and mapping of two mouse voltage-dependent anion channel isoforms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96301405;
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Mammalia; Eutheria;
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                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                  -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; PL-VDAC1 (SHOWN HERE) AND MT-VDAC1; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: HIGH LEVELS OF EXPRESSION DETECTED IN HEART,
-!- KIDNEY, BRAIN, AND SKELETAL MUSCLE. NOT EXPRESSED IN TESTIS.
-!- DOMAIN: CONSISTS MAINLY OF MEMBRANE-SPANNING SIDED BETA-SHEETS.
-!- SIMILARITY: BELONGS TO THE EUKARYOTIC MITOCHONDRIAL PORIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics 33:283-288(1996).
EMBL; U30840; AAB47777.1; -. SWISS-2DPAGE; Q60932; MOUSE. MGD; MGI:106919; Vdac1. InterPro; IPR001925; EUK_por
                                                                                          or send an email to license@isb-sib.ch).
                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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les 7; Conser
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                                                                                                                                                                                                                                                                                                                                                                       PLASMA MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282 AA;
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Rodentia;
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41.2%;
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Pred. No.
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ACETYLATION (BY SIMILARITY).
DICYCLOHEXYLCARBODIIMIDE.
; 59F77E96F108A298 CRC64;
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Sciurognathi; Muridae; Murinae; Mus
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23;
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ID KYNU_HUMAN
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PRINTS; PR00185; EUKARYTPORIN; 1.
PROSITE; PS00558; EUKARYOTIC_PORIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHOGLYCERATE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=5886;
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15-DEC-1998 (Rel.
15-DEC-1998 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 INLGCDVDFDIAGPSIR 152
                                                                                                                                                                         NON_TER
                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Paramecium
                                                                                                                                                                                                Transferase; Kinase; Glycolysis.
                                                                                                                                                                                                             Pfam; PF00162; PGK; PROSITE; PS00111; P
                                                                                                                                                                                                                                               EMBL; AF001849; AAB58241.1; -.
                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                            InterPro; IPRO01576; PGK.
                                                          259
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                                                         PTDFVCGTGLDASSPVALH
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8; Conserv
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367 AA;
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86
1
                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37, Created)
37, Last sequence update)
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KINASE (EC 2.7.2.3) (FRAGMENT).
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86 I
13
32351 MW;
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41.2%;
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42.1%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DICYCLOHEXYLCARBODIIMIDE (BY SIMILARITY).
MISSING (IN ISOFORM MT-VDAC1).
; C0710C1717063B32 CRC64;
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                                                                                                                    Score 40;
pred No.
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24;
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30;
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STANDARD;

PRT;

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ş
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C -- CATALYTIC ACTIVITY: L-3-HYDROXYKUURENINE + H(2)O = 3-
HYDROXYANTHRANILATE + L-ALANINE.

C -- COPACTOR: PYRIDOXAL PHOSPHATE.

C -- ENRYME REGULATION: INHIBITED BY O-METHOXYBENZOYLALANINE (OMBA).

C -- PARHWAY: INVOLVED IN THE BIOSYNTHESIS OF NAD COFACTORS FROM
TRYPTOPHAN THROUGH THE KYNURENINE PATHWAY.

C -- SUBUNIT: HOMODIMER (BY SIMILARITY).

C -- SUBURIT: HOMODIMER (BY SIMILARITY).

C -- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES TESTED (HEART, BRAIN
C -- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES TESTED (HEART, BRAIN
C -- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES TESTED (HEART, BRAIN
C -- TISSUE SPECIFICITY: EXPRESSED IN LIVER AND LUNG. EXPRESSED IN
C -- TISSUE SPECIFICITY.

C -- TISSUE SPECIFICITY: OF PARCENTA, LIVER AND LUNG. EXPRESSED IN
C -- TISSUE SPECIFICITY.

C -- TISSUE SPECIFICITY: SELORES IN SEVERAL CEREBRAL AND SYSTEMIC

C -- TISSUE SPECIFICITY.

C -- TISSUE SPECIFICITY: BELONGS TO THE KYNURENINASE FAMILY. SLIGHTLY RELATED

TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
                                                                 Query Match
Best Local
                                             Matches
                                                                                                                                                 MOD_RES
BINDING
SEQUENCE
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Toma S., Nakamura M., Tone S., Okuno E., Kido R., Breton J.,

Toma S., Nakamura M., Tone S., Okuno E., Kido R., Breton J.,

Avanzi N., Cozzi L., Speciale C., Mostardini M., Gatti S., Benatti L.;

"Cloning and recombinant expression of rat and human kynureninase.";

FEBS Lett. 408:5-10(1997).

1- FUNCTION: CATALYZES THE CLEAVAGE OF L-KYNURENINE (L-KYN) AND L-3-

HYDROXYKYNURENINE (L-30HKYN) INTO ANTHRANILIC (AA) AND 3-

HYDROXYKANTHRANILIC ACIDS (3-0HAA), RESPECTIVELY. HAS A PREFERENCE
FOR THE L-3-HYDROXY FORM. ALSO HAS CYSTEINE-CONJUGATE-BETA-LYASE

FOR THE L-3-HYDROXY FORM. ALSO HAS CYSTEINE-CONJUGATE-BETA-LYASE
                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alberati-Giani D., Buchli R., Malherbe P., Broger C., Lang
Koehler C., Lahm H.-W., Cesura A.M.;
"Isolation and expression of a cDNA clone encoding human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Hepatoma; MEDLINE-96314506; PubMed-8706755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          i5-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
KYNURENINASE (EC 3.7.1.3) (L-KYNURENINE HYD
                                                                                                                                                                                                                                                                               EMBL; U57721; AAC50650.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eur. J. Biochem.
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                                                                                                                                                                                                                lydrolase;
                                           Local Similarity
nes 6; Conserv
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CATALYTIC ACTIVITY: L-KYNURENINE + H(2)0 =
  GCFVGFD 11
                                                                                                                                                 Pyridoxal phosphate; Acetylation.

1 ACETYLATION (BY SIMILARITY).

276 PYRIDOXAL PHOSPHATE (BY SIMILARITY).

465 AA; 52351 MW; BDD136BE18C79EBB CRC64;
                                             Conservative
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                                                             38.1%;
85.7%;
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                                                             Score 40; DB Pred. No. 39;
                                           Mismatches
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METAL
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PRINTS; PR00802; SERUMALBUMIN.
SMART; SM00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
                                                                                                                                                                                                                                                                                                                     HSSP; P02768; 1UOR.
InterPro; IPR000264; Serum_albumin.
                                                                                                                                                                                                                                                                                                                                                                            EMBL; X60688; CAA43098.1;
EMBL; V00381; CAA23680.1;
PIR; S15571; ABCHS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-83161037; PubMed-6187737;
Hache R.J.G., Wiskocil R., Vasa M., Roy R.N., Lau P.C.K., Deeley R
"The 5' noncoding and flanking regions of the avian very low densi-
apolipoprotein II and serum albumin genes. Homologies with the egg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Liver;
Cassady A.I., Salkild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SERUM ALBUMIN PRECURSOR. ALB.
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01-AUG-1992 (Rel. 23,
01-FEB-1996 (Rel. 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
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Biochem. Biophys. Res. Commun.
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MEDLINE=78019943; PubMed=911327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        white protein genes.";
J. Biol. Chem. 258:4556-4564(1983).
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                                                                                                                            PROPEP
                                                                                                                                                                                                      Plasma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: EXTRACELLULAR.
TISSUE SPECIFICITY: PLASMA.
DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: SERUM ALBUMIN. THE MAIN PROTEIN OF PLASMA, HAS A GOOD BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES, BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
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Neognathae; Galliformes; Phasianidae; Phasianinae;
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  COPPER (BY SIMILARITY).
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                                                                                                                                                                                                   Repeat; Signal;
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RESULT PEXAL PORT OF PROPERTY 
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Best Local Similarity 54.9
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                               "The Hansenula polymorpha PER1 gene is essential for peroxisome biogenesis and encodes a peroxisomal matrix protein with both carboxy- and amino-terminal targeting signals.";
J. Cell Biol. 127:737-749(1994).

-i- FUNCTION: ESSENTIAL FOR PEROXISOME BIOGENESIS. MAY PLAY A ROLE TRIGGERING THE PROTEIN IMPORT COMPETENCE OF INDIVIDUAL PEROXISOMES. IT MAY INTERACT WITH PERB (PEX10).
                                                                                                                                                    entities re
or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CBS 4732;
MEDLINE=95050945; PubMed=7962056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=CBS 4732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pichia angusta (Yeast) (Hansenula polymorpha).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997
15-DEC-1998
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                                                                                                            EMBL; Z30206; CAA82928.1;
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                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Veenhuis M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterham H.R., Titorenko V.I., Haima P., Cregg J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                         PEROXISOMES. IT MAY INTERACT WITH PER8 (PE SUBCELLULAR LOCATION: PEROXISOMAL; MATRIX.
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PEROXISOMAL MATRIX PROTEIN PER1. MICROBODY TARGETING SIGNAL (POTENTIAL).
                                             MICROBODY.
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Best Local
                                      CHAIN
ACT_SITE
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METAL
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P49250;
   METAL
SEQUENCE
                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                     -!- PTM: THE TOPA QUINONE IS GENERATED BY COPPER-DEPENDENT AUTOXIDATION OF A SPECIFIC TYROSYL RESIDUE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE COPPER/TOPAQUINONE OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                     <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                            J. Bacteriol. -i- FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequ
15-JUL-1999 (Rel. 38, Last anno
COPPER AMINE OXIDASE PRECURSOR
                          METAL
                                                                                                                                Pfam; PF01179; Cu_amine_oxid; 1. Pfam; PF02727; Cu_amine_oxidN2; 1 Pfam; PF02728; Cu_amine_oxidN3; 1
                                                                                                                                                                            EMBL; D10208; BAA01060.1; HSSP; P46883; 10AC.
                                                                                                                                                                                                                                                                                                                                                                <del>'</del>
                                                                                                                                                                                                                                                                                                                                                                                                                        monoamine oxidase structural gene (maoA) J. Bacteriol. 174:2485-2492(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sugino H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klebsiella aerogenes
                                                                                                          PROSITE;
                                                                                                                     PROSITE;
                                                                                                                                                                  InterPro; IPR000269; Copper_amine_oxdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                             "A monoamine-regulated Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92210491; PubMed=1556068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=28451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TYRAMINE OXIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145
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                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: PERIPLASMIC. INDUCTION: BY TYRAMINE AND CATECHOLAMINES
                                                                                                                                                                                                                                                                                                                                                                COFACTOR: COPPER AND TOPAQUINONE
                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: ACTIVE ON TYRAMINE,
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7; Conser
                                                                                           PS01165; COPPER_AMINE_OXID_1; 1.
PS01165; COPPER_AMINE_OXID_2; 1.
nctase; Copper; TPQ; Periplasmic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sasaki M., Azakami H.,
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                31
413
496
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                                                                                   Copper;
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36
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"""CAR (EC 1.4.3.6) (N
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     X.
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    COPPER AMINE OXIDASE.
CATALYTIC BASE (BY SIMILARITY).
TOPAQUINONE (BY SIMILARITY).
COPPER (POTENTIAL).
COPPER (POTENTIAL).
COPPER (POTENTIAL).
COPPER (POTENTIAL).
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aerogenes
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eron containing
he maoC gene.";
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Matches 8: Conservative 4: At.s. Pred. No. 63:

Matches 9: Conservative 4: Atlanatches 6: Indels 0: Gaps 0:

Oy 1 PVSVGCPVGFDASEDDAR 18

Db 254 PLTVGFTDAKGLGDDAR 271

Search completed: November 30, 2001, 09:40:55

Job time: 34 soc
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                       sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                          sp_rodent:*
sp_virus:*
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 BB
   Q9XEQ8
Q9GZF1
023053
080885
                                     Q9C5NO
Q63709
Q9AV10
Q9MCH9
Q9U249
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Q9VVQ2
Q9LZ54
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Q9M4M7
Q82796
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Q9QVW8
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Q9zt62 cucumis sat
Q9m4m7 persea amer
O82796 arabidopsis
Q9fz85 arabidopsis
Q9fz85 arabidopsis
Q9fz85 arabidopsis
Q9fz86 arabidopsis
Q9fz87 aratus sp.
Q4942 mycobacteri
Q9vvq2 drosophila
Q91254 arabidopsis
Q63709 rattus sorv
Q9av10 oryza sativ
Q9av10 oryza sativ
Q9mv10 caenorhabdi
Q9xeq8 sorghum bic
Q9zfi caenorhabdi
Q3053 arabidopsis
Q80885 arabidopsis
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aner sound newish	TZ CATMAC	139	39.0	4	40
Ogtwan nothog	12 09TWAO	720	30.0	۱.	л.
020329 caenorhabd1	5 020329	552	39.0	41	44
Q9a4c3 caulobacter	2 Q9A4C3	511	39.0	41	43
Q23017 caenorhabdi	5 Q23017	314	39.0	41	42
Q9mz16 sus scrofa	6 Q9M216	283	39.0	41	41
Q9x3x6 zymomonas	2 Q9X3X6	251	39.0	41	40
Q9js17 neisseria	2 Q9JS17	125	39.0	41	39
Q9p8b3 agaricus bi	3 Q9P8B3	360	39.5	41.5	38
Q9fmb0 arabidopsis		222	39.5	41.5	37
039302 equine herp		219	39.5	41.5	36
Q9x4m7 lactobaci		101	39.5	41.5	35
Q9ayh7 oryza sativ		1132	40.0	42	34
Q9a2e5 caulobacter		653	40.0	42	33
Q9m8z4 arabidopsis		648	40.0	42	32
Q9xus4 caenorhabdi	5 Q9XUS4	511	40.0	42	31
O52785 acinetobact		439	40.0	42	30
008410 shewanella	2 008410	419	40.0	42	29
Q91ch6 streptomyce		393	40.0	42	28
Q9fvh5 prunus arme		376	40.0	42	27
Q9xw86 caenorhabdi		314	40.0	42	26
O44789 caenorhabdi		311	40.0	42	25
Q51720 propionibac	2 Q51720	257	40.0	42	24
Q9kbf5 bacillus h		240	40.0	42	23
Q9yb34 aeropyrum	1 Q9YB34	169	40.0	42	22
031813 bacillus	2 031813	546	40.5	42.5	21
Q9cxf0 mus musculu	11 Q9CXF0	464	41.0	43	20

ALIGNMENTS

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RESULT
Q9M4M7
ID QS
AC QS
DT 01
DT 01
DT 01
DT 01
DT 03
GN S3
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Best Local S
Matches 19
PUTATIVE SIP.
                       Q9M4M7 PRELIMINARY; PRT; 779 AA.
Q9M4M7;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                               TISSUE-LEAF;
Obsumi C., Nozaki J., Kida T.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF073744; AAD02832.1;
Transferase; Glycosyltransferase.
SEQUENCE 784 AA; 86919 MW; 3B06A491F0908933 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    Cucumis sativus (Cucumber).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q92T62 PRELIMINARY; PRT; 784 AA.
Q92T62;
Q1-MAY-1999 (TrEMBLrel. 10, Created)
Q1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
Q1-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RAFFINOSE SYNTHASE (EC 2.4.1.82).
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3659;
                                                                                                                                               61
                                                                                                                                             l Similarity
19; Conserva
            SEED
                                                                                                                                                                                                 Conservative
             IMBIBITION PROTEIN.
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Pred. No. 1.1e-08;
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ID Q9F285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

HO C., Noji M., Saito K.;

"Molecular cloning and characterization of PSP.";

"Molecular cloning and characterization of PSP.";

Submitted (CCT-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AB018409; BAA33807.1; -.

EMBL; AB018408; BAA33806.1; -.

InterPro; IPR001454; Hydrolase.

Pfam; PF00702; Hydrolase; 1.

SEQUENCE 295 AA; 32302 MW; F14C95E636E6754E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O82796 PRELIMINARY; PRT; 295 AA.
082796;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
3-PHOSPHOSERIN PHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zamorano J.P., Evans A.D., Dopico B., Lowe A.L., Wilson I.D., Merodio C., Grierson D.;
Merodio C., Grierson D.;
Tolation and characterization of cDNAs for mRNAs regulated cold storage of avocado (Persea americana Mill.) fruit.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ133148; CAB77245.1;
SEQUENCE 779 AA; 85368 MW; C3A8B43160316785 CRC64;
                            Arabidopsis thaliana (Mouse-ear cress). Embry Eukaryota; Viridiplantae; Streptophyta; Embry Spermatophyta; Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Persea americana (Avocado)
Eukaryota; Viridiplantae;
  Spermatophyta; eurosids II; B:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3702;
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NCBI_TaxID=3435;
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nes 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
  a; Magnoliophyta;
Brassicales; Bras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Magnoliophyta;
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yta; Laurales;
     Brassicaceae;
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Pred.
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                                                     Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10;
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     Arabidopsis.
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                                 core eudicots;
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ID Q9YHD2

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                                                                                                 O9YHD2
O9YHD2:
O1-MAY-1999 (TrEMBLrel. 10, Cr.
T 01-MAY-1999 (TrEMBLrel. 10, La
JT 01-JUN-2001 (TrEMBLrel. 17, La
MICLEAR CALMODULIN-BINDING PR
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Best Local S
Matches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structural analysis of Arabidopsis thaliana of Sequence features of the regions of 1,044,062 physically assigned Pl clones.";
DNA Res. 4.291-300(1997).
EMBL; AB006702; BAB11595.1; -.
SEQUENCE 783 AA; 86237 MW; 3C37D1D7871888/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-COLUMBIA;
MEDLINE-98069011; PubMed-9405937;
Kotani H., Nakamura Y., Sato S., I
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eddicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9FND9 PRELIMINARY; PRT; 783 AA.
Q9FND9;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
RAFFINOSE SYNTHASE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S., Buehler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A., Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M., Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P., Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.; submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

EMBL; AC026238; AAF98410.1; -
                                                                     Gallus gallus (Chicken).
Eukaryota: Metazoa; Chordata;
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[1]
                                               Archosauria;
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Local :
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10; Conservative
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                                                 Aves;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.3%;
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PROTEIN (FRAGMENT).
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Pred.
                                                    Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3C37D1D7871888AC
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edons; core eudicots; Rosid
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                                                      Phasianinae;
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RESULT
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DT 01
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MI
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2 049942
3 049942;
C 049942;
C 049942;
T 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-VOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-VOV-2001 (TrEMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 33.9 KDA PROTEIN L518_F3_81.
GN ML2346 OR L518_F3_81 OR MLCB2407.04.
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Matches 7
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Best Local
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SEQUENCE FROM N.A.

MEDLINE-94293355; PubMed-8021968;

Yazaki N., Hosoi Y., Kawabata K., Miyake A., Minami Yazaki N., Hosoi Y., Itoh N.;

Ohta M., Kawasaki T., Itoh N.;

"Differential expression patterns of mRNAs for membranching arowth factor receptor family, FGFR-1-FG
                                                                                                                                                                                                                                                                                                         HSSP; P06239; 3LCK:
InterPro; IPRO0719; Euk_pkinase.
Pfam; PP00069; pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS00111; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O9QVW8 PRELIMINARY; PRT;
O9QVW8;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2001 (TrEMBLrel. 13, Last sequ
O1-JUN-2001 (TrEMBLrel. 17, Last anno
FIBROBLAST GROWTH FACTOR RECEPTOR 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to HnRNP-U.", Submitted (OCT-1998) to the EMBL/ EMBL; AF098788; AAC69888.1; -. InterPro; IPR003877; SPRY. InterPro; IPR003878; SPRY_domain. Pf6am; PF00622; SPRY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID-10118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 ATP-binding; II.... 202 AA;
                                                                                                                                                                                                                                                                                                                                                                           J. Neurosci. Res.
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                                                                                                                                                                                                                          Similarity
9; Conserv
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Similarity 53.8%;
7; Conservative
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f ChURP, a Nuclear
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                                                                                                                                                                                                                                                                                        21986 MW;
                                                                                                                                                                                                                                     41.9%;
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Last annotation update)
CEPTOR 4, FGFR-4.
                                                                                                                                                                                                                        Score 44; DB Pred. No. 21; 3; Mismatches
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                                                                                                                                                                          172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                       8F87690566EBFA31 CRC64;
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Calmodulin-Binding Protein
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Best Local
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O9VVQ2;
01-MAY-2000 (
01-MAY-2000 (
01-MAY-2000 (
CG7271 PROTE)
CG7271.
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Robison K., Smith D.I
Submitted (MAR-1994)
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STRAIN-BERKELEY;

MEDLINE=20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D. Ananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly),
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein. seQUENCE 301 AA; 33939 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE=93188700; PubMed=8446027;

Eiglmeier K., Honore N., Woods S.,

Eiglmeier K., 197-206(1993).

MOI. Microbiol 7:197-206(1993).

EMBL; AL583925; CAC31862.1; -.

EMBL; U00023; AAA17366.1; -.
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Seeger K., Harris D.;
Submitted (MAY-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Squares S.,
Barrell B.G
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Massive gene decay in the leprosy bacillus."; Nature 409:1007-1011(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AL023596; CAA19144.1; -.
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8; Conserv
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(MAY-1998)
                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 13,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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to the
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57.1%;
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e EMBL/GenBank/DDBJ
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Pred. No. 32;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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a; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                      update)
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RA Ballew R.M. Basu A. Basundie J. Bayraktaroglu L. Beasley E.M.,
RA Besson K.Y. Bengs P.V. Berman B.P. Bhandari D., Bolshakov S.,
RA Besson K.Y. Bengs P.V., Berman B.P. Brokstein P., Bolshakov S.,
RA Besson K.Y. Bengs P.V., Berman B.P. Brokstein P., Bolshakov S.,
RA Bersis K.C. Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Glori K.C. Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Glori K.C. Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Glori K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.,
RA Rainzolo M., Pittman G.S., Pan S., Pollard J., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shie B.C., Siden-Riamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Riamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Riamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Riamos I.A., Weilsenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weilsen K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhong M., Zhou X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhong M., Zhou X., Smith H.O.,
RA Schiese Sequence of Drosophila melanogaster.";
RT The genome sequence of Drosophila melanogaster.";
RT The genome sequence of Drosophila melanogaster.";
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Best Local S
Matches 7
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01-JUN-2001 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TYPOTHETICAL 55.5 KDA PROTEIN.
T25P11-70.
               SEQUENCE FROM N.A.

EU Arabidopsis sequencing project;

EU Arabidopsis sequencing project;

Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases

EMBL; AL162971; CAB85985.1; ...
                                                                                                                     Bevan M., Hilbert H.,
Bancroft I., Mewes H.,
Submitted (APR-2000)
                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 7; Conserv
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                                                                                                                     Braun M., Holzer E., Bra
W., Rudd S., Lemcke K., M
to the EMBL/GenBank/DDBJ
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Pred. No.
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Nelson C.R., Miklos (
                                                                                                                                           Brandt A., Dues
                                                                                                                              databases
                                                                                                                                                                                                                                                                          core eudicots; Rosidae;
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                                                                                                                                                                     Duesterhoeft
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G.L.G.,
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RESULT Q63709 ID Q63709 OC F COX F P C
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PROSITE; PS01013; CARBOXYPE;
PROSITE; PS01031; HSP20; 1.
Hypothetical protein.
SEQUENCE 498 AA; 55530 M
                                                                                                                                                                                                                                                                                                                                                                                                         Q63709
Q63709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002068; Crystallin_HSP20.
InterPro; IPR000834; Zn_carbOpept.
PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
PROSITE; PS01031; HSP20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Full Length cDNA of gene T22P11.70/AT5g02480 (GI:7413637)."; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF360137; AAK25847.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M., Goldsmith A.D., Lee J.M., Quach H., Toriumi M., Yu G., Bow Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., J Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Eseki M., Shinn P., Southwick A., Shinozaki K., Davis R.W.,
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Eukaryota; Viridiplantae; Strotophyta; Embryophyta;

Eukaryota; Viridiplantae; eudicotyledons; core eu

Spermatophyta; Magnoliophyta; eudicotyledons; core eu

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-JUN-2001 (TrEMBLIEL 17, La
01-JUN-2001 (TrEMBLIEL 17, La
HYPOTHETICAL 56.6 KDA PROTEIN.
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                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein SEQUENCE 508 AA;
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                                                                                                                                                                                 FGFR4.
Rattus norvegicus (Rat).
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   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                         FIBROBLAST GROWTH
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7; Conserv
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PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
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70.0%;
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                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 498
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Jones T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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RESULT 14
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AC Q9MCH9
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Best Local S
Matches 9
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R HSSP; P06239; 3LCK.

R INTETPTO; IPR003798; Ig_C2.

R InterPro; IPR003598; Ig_C2.

R InterPro; IPR00306; Ig_MHC.

R InterPro; IPR00306; Ig_MHC.

R InterPro; IPR00306; Tyr_kin.

R Pfam; PF00069; pkinase; 1.

R PFRNTS; PR00109; TYRKINASE.

R SMART; SM00408; IGC2; 2.

R SMART; SM00219; TyrKC; 1.

R PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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Q9MCH9;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN-CV. NIPPONBARE;

Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Burr P.C.,

Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Burr P.C.,

L., Crawen B., Utterback T.R., Khalak H., Feldblyum T.V.,

Quackenbush J., White O., Salzberg S.L., Fraser C.M.;

Quackenbush J., White O., Salzberg S.L., Fraser C.M.;

"Oryza sativa Chromosome 10 BAC OSJNBb001411 genomic sequence.";

Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AC037426; AAK15443.1;

EMBL; AC037426; AAK15443.1;

BBEEF530901BD055 CRC64;
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O9AV10, 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (Rice).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoidese; Oryzeae; Oryza.
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-I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4530;
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nes 8; Conserv
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Pred. No. 71;
                                 PRT;
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                                               Query Match
Best Local Similarity
Matches 7; Conserv
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Q9U249;
01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, L
01-MAR-2001 (TrEMBLrel. 16, L
Y53H1B.4 PROTEIN.
                                                                                                 "Genome Sequential Tributes of the Science 282:2012-2018(1998).

EMBL; AL132851; CAB60412.1; -.

EMBL; AL132851; CAB60412.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Desiere F., Lucchini S., Bruessow H.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF158600; AAF63067.1; -.
InterPro; IPR001387; HTH_3.
Pfam; PF01381; HTH_3; 1.
SMART; SM00530; HTH_XRE; 1.
SMART; SM00530; HTH_XRE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lucchini S., Desiere F., Brussow H.; "Comparative genomics of Streptococcus supports a modular evolution theory."; J. Virol. 73:8647-8656(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE DNA BINDING PROTEIN.
Streptococcus thermophilus bacteriophage Sfill.
Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae.
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                          Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-99412383; PubMed-10482618;
                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       Y53H1B.4.
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                                                                                                                                                                          MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                        White S.
                                                                                                                                                                none;
       117
                                                                                                                                                    Genome sequence of the nematode
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CFVGFDASEPDSRH 19
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9; Conserv
                                                                                                                                                                                                           (JUN-1999)
                                                 Conservative
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Search completed: November 30, 2001, 09:44:54

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Copyright (c) 1993 - 2000 Compugen
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1 PVSVGCFVGFDASEPDSRH	Match Ocal Simi s 19;	NAME: NORMAN F. OBLON REGISTRATION NUMBER: 24,618 TELECOMMUNICATION INFORMATION: TELEPHONE: (703)-413-3000 TELEFAX: (703)-413-220 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 19 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: peptide FRAGMENT TYPE: internal 08-846-234-2	COUNTRY USA ZIE: 22202 ZIE: 22202 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DO SOFTWARE: Patentin Release #1. CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/846, FILING DATE: APTERNEY CAFFUT TUPORMATION:	IUMBER OF SEQUENCES: CORRESPONDENCE ADDRE ADDRESSEE: OBLON, STREET: 1755 S. J CITY: ARLINGTON STATE: VIRGINIA	e 2, App No. 6166 L INFORM ICANT: ICANT: ICANT: E OF INV	1 6-234-2	39 37.1 39 37.1 39 37.1 39 37.1 39 37.1 39 37.1 39 37.1 39 37.1 39 37.1 39 37.1	
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	Score 105; Pred. No. 1. ; Mismatches	.: ∞	e S-DOS #1.0, Version 846,234	CLELLAND, NVIS HIGHWA	34 SYNTHASE RAFFINOSE	ALIGNMENTS	PCT-US95-14418-5 PCT-US95-15327-5 PCT-US95-15418-4 PCT-US95-15327-4 US-08-073-384C-8 US-08-254-359A-8 US-08-481-238-8 US-08-481-238-8 US-08-471-066B-8 US-08-484-956-8	CT-US91-07035 CT-US91-07035 CT-US95-14411 CT-US95-15327 CT-US95-15327 S-08-338-5307 S-08-357-384 S-07-857-2241
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Best Local S
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               Sequence 460, Application US/08905223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: OSUMI Chieko
APPLICANT: NOZAKI Jinshi
APPLICANT: KIDA Takao
TITLE OF INVENTION: RAFFINOSE SYNTHASE GENE, METHOD FOR
TITLE OF INVENTION: PRODUCING RAFFINOSE, AND TRANSGENIC PLANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703)-413-2220 INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,234
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
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                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                              NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                    APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR CITY: ARLINGTON STATE: VIRGINIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PVSVGCFVGFDASEPDSRH 79
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nes 19; Conserv
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                                                                                   COUNTRY: USA
ZIP: 92101-3505
                                                                                                                                           CITY: San Diego
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             COMPUTER: IBM PC compation OPERATING SYSTEM: Win95
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SOFTWARE:
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                                                                                                                         California
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FEATURE:
NAME/KEY: SITE
LOCATION: (136)
OTHER INFORMATION: Xaa-unknown amino acid
US-08-861-774E-22
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                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/08/861,774E
CURRENT FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 94
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22, Application US/08861774E Patent No. 6297007
                                                                            Query Match
Best Local :
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TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 460
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Waters, Barbara
APPLICANT: Miao, Vivian
APPLICANT: Ho, Yap
APPLICANT: Tong, Seow
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: TONG, SOOW
TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR
TITLE OF INVENTION: BIOACTIVE MOLECULES
FILE REFERENCE: 9993-006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
NOTITION NUMBER: US/08/905,223
                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                            ORGANISM: Xanthoparmelia cumberlandia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: I ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
                                                                                                                                                                                                                                                           ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: sig_peptide
LOCATION: -17..-1
IDENTIFICATION METHOD: Von Heijne matrix
OTHER INFORMATION: score 5.2
OTHER INFORMATION: seq IMCLIGLKANASS/ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE TYPE:
                                                           Local Similarity hes 7; Conserv
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22
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                             1 PVSVGCFVGFDASEPD 16
 PEDVGCYIGACATDYD 37
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E: PROTEIN
                                                                Conservative
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                                                                               39.0%;
43.8%;
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                                                                               Score 41; DB Pred. No. 30;
                                                                  Mismatches
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                                                                                               Length 212;
                                                                   Indels
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TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES
TILLE OF INVENTION: BIOACTIVE MOLECULES
FILE REFERENCE: 9993-006
CURRENT APPLICATION NUMBER: US/08/861,774E
CURRENT FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 94
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 34
LENGTH: 212
TYPE: PRT
ORGANISM: Leptoglum corniculatum
US-08-861-774E-34
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Best Local Similarity
""" Conserve
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US-08-861-774E-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09105697 Patent No. 6228628
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                                                                                      REFERENCE/DOCKET NUMBER: 1043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510)814-2974
TELEFAX: (510)814-2977
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Waters, Barbara
APPLICANT: Mimo, Vivian
APPLICANT: Ho, Yap
APPLICANT: Tong, Seow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,697
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC competible

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reichert, Fred L.
TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gelfand Ph.D., David H. APPLICANT: Reichert, Fred L.
MOLECULE TYPE: protein -105-697-4
                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Petry Ph.D., Douglas A.
REGISTRATION NUMBER: 35321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Roche Molecular Systems STREET: 1080 U.S. Highway 202 CITY: Branchburg
                                    STRANDEDNESS: Sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: UI
ZIP: 08876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 PEDVGCYIGACATDYD 37
                                                                      TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Jersey
: United States
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                                                  single
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Pred. No.
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US-09-105-697-6

Sequence 6, Application US/09105697

Patent No. 6228628

; GENERAL INFORMATION:
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Best Local S
Matches 8
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (510)814-297
TELEPAX: (510)814-2977
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
        APPLICANT: Gelfand Ph.D., David H.
APPLICANT: Reichert, Fred L.
TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gelfand Ph.D., David H.
APPLICANT: Reichert, Fred L.
TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Petry Ph.D., Douglas A.
REGISTRATION NUMBER: 35321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Branchburg
STATE: New Jersey
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 FVVFDAKAPSFRH 76
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tes 8; Conserv
                                                                                                                                                                                                             64 FVVFDAKAPSFRH 76
                                                                                                                                                                                                                                                                         Local Similarity 61.
                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 1
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
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1080 U.S. Highway 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (510)814-2977
OR SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                                                                                                            linear
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Roche Molecular Systems
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; Pred. No. 62;
0; Mismatches
                                                                                                                                                                                                                                                                         Score 40; DB pred. No. 62; 0; Mismatches
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                                                                                                                                                                                                                                                                                                           DB 4;
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-105-697-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-07-977-434-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Geliand, Dark....
APPLICANT: Abramson, Richard D.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Petry Ph.D., Douglas A.
REGISTRATION UNMBER: 35321
REFERENCE/DOCKET NUMBER: 1043
                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 590,490
                                                                                                                                                                                 OPERATING SYSTEM: 7
SOPTWARE: WordPerfect 2.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07,
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,466
FILING DATE: 28-SEP-1990
                                                                                                                                                                                                                                                                                                             STREET: 340 Kingsle
CITY: Nutley
STATE: New Jersey
ZIP: 07110-1199
               PRIOR APPLICATION DATA:
                                                                                      APPLICATION NUMBER: US 59 FILING DATE: 28-SEP-1990
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nes 8; Conserv
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                                                                                                                                                                                                                                                           COMPUTER:
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(510)814-2977
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linear
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US 590,213
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-07-977-434-8
                                                                                                                                                                                                                                                                              RESULT 10
US-07-977-434-10
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Best Local Similarity o...
Best Focal Similarity
Conservative
                                                                                                                                                                                                                                          Sequence 10, Application US/07977434
Patent No. 5466591
                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Gelfand, E
APPLICANT: Abramson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 17-JUN-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS LENGTH: 834 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: Ca
TELECOMMUNICATION INFORMATION:
                                                                                                                                                       APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 02-NOV-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 22-DEC-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Luann Cserr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 70
                                                                                                                                                                                                                                                                                                                                                   64 FVVFDAKAPSFRH 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 50 STITLING DATE: 20-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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                                  STATE: New Jersey ZIP: 07110-1199
                                                                      CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: WO PCT/US90/07641 FILING DATE: 21-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                    STREET:
                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               834 amino acids
                                                                                    340 Kingsland Street
                                                                                                                                                                                                             Gelfand, David H
                                                                                                        Hoffmann-La Roche Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (510)
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22-AUG-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 1;
Pred. No. 2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 834;
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COMPUTER: Macinto OPERATING SYSTEM:

Macintosh

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RESULT 11
US-08-073-384C-6
; Sequence 6, Application US/08073384C
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                                                                                                                                                                                   Query Match
                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                        NFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 15-MAY-1S
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 834 amino acid
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APPLICATION NUMBER: US 455,611
FILING DATE: 22-DEC-1989
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APPLICATION NUMBER: US/07/977,434
                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 02-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 609,157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: WO PCT/US90
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 585,471
FILING DATE: 20-SEP-1990
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APPLICATION NUMBER: US 746,121
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                                                                                                                                    Local Similarity
nes 8; Conserv
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                                                                                     62
                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                   NAME: Luann Cserr
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: Case No. 5466591 8753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 063,509 FILING DATE: 17-JUN-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 557,517 FILING DATE: 24-JUL-1990
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                                                                                                                                                                                                                                                                                                                                                           TELEPHONE
                                                                                                        7 FVGFDASEPDSRH 19
                                                                                     FVVFDAKAPSFRH 76
                                                                                                                                                                                                                                                                                                      834 amino acids
                                                                                                                                                    Conservative
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28-SEP-1990
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12-JAN-1988
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21-DEC-1990
                                                                                                                                                                     38.1%;
61.5%;
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                                                                                                                                                                     Score 40;
Pred. No.
                                                                                                                                                    Mismatches
                                                                                                                                                                       2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 415/705-84
TELEFAX: 415/397-8338
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 834 amino acids
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                                                                                                                                                                 APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: BROW, MARY AND VICTOR I.
TITLE OF INVENTION: 5' NUCLEASES DERIVED FROM THERMOSTABLE
TITLE OF INVENTION: DNA POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 1:
MOLECULE TYPE:
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                  APPLICANT:
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                                                                   CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 04-JUN CLASSIFICATION: 536
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                     64 FVVFDAKAPSFRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Carroll, Peter G. REGISTRATION NUMBER: 32,837 REFERENCE/DOCKET NUMBER: FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                     COUNTRY:
                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 Montgomery Street, Suite 2200
                                                                                                   E: HAVERSTOCK, MEDLEN & CARROLL 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brow, Mary Ann D.
                                                   UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lyamichev, Victor I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dahlberg, James E.
                                                                                                                                                                                                                                  DAHLBERG, JAMES E.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WUMBER: US/08/073,384C
04-JUN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    38,1%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 834;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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RESULT 13
US-08-384-490-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gelfand, David H.
APPLICANT: Lawyer, Frances C.
APPLICANT: Stoffel, Susanne
TITLE OF INVENTION: Recombinal
TITLE OF INVENTION: purificat
TITLE OF INVENTION: Polymeras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 397-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REGISTRATION NUMBER: FORS-01000
REFERENCE/DOCKET NUMBER: FORS-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410]
TELEFAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/986,330 FILING DATE: 07-DEC-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/148,133
                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 834 amino acids TYPE: amino acid STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/254,359A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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mes 8; Conserva
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                                                                                                                                                                                                                                                                                 STATE: New Jersey COUNTRY: U.S.A. ZIP: 07110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                       CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                         STREET:
NAME: Sias, REGISTRATION
                                                    FILING DATE:
                                                                                                             CLASSIFICATION: 435
                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 FVGFDASEPDSRH 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l, Application US/08384490 5618711
                                                                                                                                                                                                                                                                                                                                                         340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lawyer, Frances C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Stacey R.
NUMBER: 32,630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.1%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant Expression Vectors and Purification Methods for Thermus Thermophilus DNA
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Pred. No.
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Query Match

38.1%;

Score 40;

DB 1;

Length 834;

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RESULT 14
US-08-483-043-6
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; MOLECULE TYPE: US-08-483-043-6
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                  TELEFAX: 415/397-8338
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 834 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dahlberg, APPLICANT: Lyamichev APPLICANT: Brow, Mar TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 88
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2863
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                     REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                        FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 04-JUN-1993
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94104
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco
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TOPOLOGY: lir
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                                                      STRANDEDNESS:
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                                      TOPOLOGY:
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Brow, Mary Ann D.
                                                                                      834 amino acids
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Pred. No. 2e+02;
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STREET: NUTLEY
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/459,383
FILING DATE:
CLASSIFICATION NUMBER: US/08/459,383
FILING DATE:
APPLICATION NUMBER: US/08/148,133
FILING DATE:
APPLICATION NUMBER: US/08/148,133
FILING DATE:
APPLICATION NUMBER: US/08/148,133
FILING DATE:
APPLICATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 8887
TELECOMMUNICATION INFORMATION:
TELEPHAN: (510) 814-2863
TELEFOAN: (510) 814-2977
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 834 amilno acids
TYPE: amilno acids
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US-08-459-383-31
Search completed: November 30, 2001, 09:43:38 Job time: 197 sec
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Matches 8; Conservative
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Best Local Similarity 61.5%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gelfand, David H.
APPLICANT: Lawyer, Frances C.
APPLICANT: Stoffel, Susanne
TITLE OF INVENTION: Recombinant Expression Vectors and
TITLE OF INVENTION: Purification Methods for Thermus Thermophilus DNA
TITLE OF INVENTION: Polymerase
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 FVVFDAKAPSFRH 76
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0; Mismatches
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                    Score
   length: 0
length: 2000000000
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                   Query
Match
                                                                                                                                                                                                                                                                                                                                                A_Geneseq_1101:*

/SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*

/SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*

/SIDSB/gcgdata/geneseq/geneseqp/AA1982.DAT:*

/SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*

/SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*

/SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*

/SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*

/SIDSB/gcgdata/geneseq/geneseqp/AA1987.DAT:*

/SIDSB/gcgdata/geneseq/geneseqp/AA1987.DAT:*

/SIDSB/gcgdata/geneseq/geneseqp/AA1987.DAT:*

/SIDSB/gcgdata/geneseq/geneseqp/AA1997.DAT:*

/SIDSB/gcgdata/geneseq/geneseqp/AA1997.DAT:*

/SIDSB/gcgdata/geneseq/geneseqp/AA1997.DAT:*

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     AAB98659
AAW57887
AAY30143
AAB49400
AAG53157
AAG53156
AAY32075
                                                                                                                       AAW53569
AAY17424
AAW53570
AAY17417
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14.781 Million cell updates/sec
        Cucumber raffinose Cucumber raffinose Cucumber raffinose Cucumber raffinose Soybean protein: Soybean raffinose Amino acid sequenc Soybean raffinose Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia
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Cucumber raffinose
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); 26pp; Japanese. Noe is a cucumber raff oforms raffinose from	ase gene - useful for prent	OTO KK.	96JP-0198079. 96JP-0107682.	97JP-0111124.		·	nose synthase; sucrose, se	residues /30			rd; peptide; 14 AA.	ALIGNMENTS	586 21 AAG53155 777 20 AAY32074 228 21 AAG07534 229 21 AAG07533 229 21 AAG45845 269 21 AAG45845 270 21 AAG52085 637 21 AAG52085 637 21 AAG52083 673 21 AAG52083 854 22 AAM42222 864 22 AAM42222 864 22 AAM42222 877 22 AAM42223 877 22 AAM42233 877 22 AAM42233
inose synthase fragment. sucrose and galactinol, has	paration of raffinose in							<u> </u>					Arabidopsis thalia Mustard raffinose Arabidopsis thalia Soybean raffinose soybean rafil toyos soybean rafil lee a Soybean rafil lee a Soybean rafil lee a Soybean rafil toyos soybean rafil toyos soybean rafil toyos soybean rafil pekin soybean rafil pekin soybean rafil pekin soybean rafil pekin soybean rafil toyos poptide #735 enco Peptide #735 enco Peptide #735 enco Arabidopsis thalia

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Db
                    RESULT
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                                                                                                                                                                               RESULT
AAY17424
                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 14; Conserv
AAW53570;
              AAW53570 standard; Protein;
                                                                                                                                                                                                 The present invention describes a raffinose synthase, having an activity of forming raffinose from sucrose and galactinol. The raffinose synthase gene can be used for expression in a plant for the production of raffinose. The raffinose synthase can give raffinose from sucrose and galactinol efficiently. The present sequence represents a raffinose
                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                             Example 2; Page 22; 37pp; Japanese.
                                                                                                                                                                                                                                                                                               New raffinose synthase gene - for production of raffinose from sucrose and galactinol % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                       WPI; 1999-340516/29.
                                                                                                                                                                                                                                                                                                                                                                                   24-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                            (AJIN ) AJINOMOTO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cucumber raffinose synthase peptide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                         24-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                11-мау-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP11123080-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cucumis sativus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY17424 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY17424;
                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an optimum pH of 6 to 8 and working temperature of 35 to 40 degrees C. has a molecular weight of 75 to 95 kDa by gel filtration or 90 to 100 kDa by PAGE and SDS-PAGE under reductive conditions and is inhibited by iodoacetamide, N-ethylmaleimide and myoinositol.
                                                                                    1 YDQDQMVVVQVPWP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                            ė
                                           w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YDQDQMVVVQVPWP 14
                                                                         ydddmvvvdvpwp 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N
                                                                                                                    ch 100.0%;
1 Similarity 100.0%;
14; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ydqdqmvvvqvpwp 14
                                                                                                                                                                              14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; ilarity 100.0%; Conservative 0;
                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                               97JP-0292969.
                                                                                                                                                                                                                                                                                                                                                                                                      97JP-0292969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sucrose; galáctinol.
                 784
                                                                                                                    0;
                                                                                                                            Score 80;
Pred. No.
                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 80; DB 19;
Pred. No. 9.9e-08;
Mismatches 0;
                                                                                                                  Mismatches
                                                                                                                9.9e-08;
ches 0;
                                                                                                                                        DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NO: 3.
                                                                                                                                    Length 14;
                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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AAY17417
                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
       WPI; 1999-340516/29
N-PSDB; AAX61238.
                                 (AJIN ) AJINOMOTO KK.
                                                    24-OCT-1997;
                                                                     24-OCT-1997;
                                                                                                          JP11123080-A.
                                                                                                                                            Raffinose synthase;
                                                                                        11-MAY-1999.
                                                                                                                            Cucumis sativus.
                                                                                                                                                               Cucumber raffinose synthase
                                                                                                                                                                                29-JUL-1999 (first entry)
                                                                                                                                                                                                                     AAY17417 standard; Protein;
                                                                                                                                                                                                       AAY17417;
                                                                                                                                                                                                                                                                                                                                                                         The present sequence is cucumber raffinose synthase, which forms raffinose from sucrose and galactinol, has an optimum pH of 6 to 8 and working temperature of 35 to 40 degrees C, has a molecular weight of 75 to 95 KDa by gel filtration or 90 to 100 kDa by PAGE and SDS-PAGE under reductive conditions and is inhibited by
                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                    756 ydqdqmvvvqvpwp 769
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Pages 17-20; 26pp;
                                                                                                                                                                                                                                                                                                                                                                   iodoacetamide, N-ethylmaleimide and myoinositol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Raffinose synthase gene - useful for preparation of raffinose transformed plant % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAV22250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUL-1996;
26-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AJIN ) AJINOMOTO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JP10084973-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cucumis sativus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cucumber; raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cucumber raffinose synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                             1 YDQDQMVVVQVPWP 14
                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1998-264858/24
                                                                                                                                                                                                                                                                                                      Similarity 100.
14; Conservative
                                                                                                                                                                                                                                                                                                                                                      784 AA;
                                                   97JP-0292969
                                                                    97JP-0292969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96JP-0198079
96JP-0107682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97JP-0111124
                                                                                                                                           sucrose; galactinol.
                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                       784
                                                                                                                                                                                                                                                                                                   Score 80; DB Ly; Pred. No. 8.8e-06;
                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sucrose; galactinol.
                                                                                                                                                                                                                      AA
                                                                                                                                                                                                                                                                                                                       Length 784;
                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                    0;
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RESULT
AAB98659
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Best Local
                                                  Query Match
Best Local
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                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene can be used for expression in a plant for the production of raffinose. The raffinose synthase can give raffinose from sucrose and galactinol efficiently. The present sequence represents raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a raffinose synthase, having an activity of forming raffinose from sucrose and galactinol. The raffinose synthase
                                                                                                                         the
                                                                                                                                 The present invention relates to a mutant protein of raffinose synthas, in which at least one aromatic amino acid present at the position of about 1-7 amino acids from the N-terminus is deleted or replaced. The mutant protein can be used for reducing the raffinose oligosaccharide content in a plant body. The present protein from soybean, was used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sucrose and
                                                                                                                                                                                                                                   Novel mutant protein of raffinose synthase is useful for reducing the raffinose oligosaccharide content in a plant body - {\sf raff}
                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soybean protein:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB98659 standard; protein; 780 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthase from cucumber.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New raffinose synthase gene · for production of raffinose from sucrose and galactinol
                                                                                                 Sequence
                                                                                                                                                                                                           Disclosure; Page 18-20; 30pp; Japanese.
                                                                                                                                                                                                                                                                                                                                        09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                               03-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                        27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                JP2001078783-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB98659
                                                                                                                                                                                                                                                                                                              (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       756 ydqdqmvvvqvpwp 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YDQDQMVVVQVPWP 14
            w
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                                                                                                                        present invention.
QDQMVVVQVPWP 14
:|:|: ||||||
                                                                                                                                                                                                                                                                                       2001-313373/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               soybean
                                    Similarity 66.3
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutein; raffinose synthase; raffinose oligosaccharide reduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 25-27; 37pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      784 AA;
                                                                                                 780 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                               2000JP-0200571.
                                                                                                                                                                                                                                                                                                                                       99JP-0196036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                              Score 50; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 80; DB 20;
Pred. No. 8.8e-06;
                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                            DB 22;
                                                 .
6
                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                           Length 780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                    0
                                                                                                                                                                                     synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                    0
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RESULT
AAY30143
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AAW57887
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                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                          This sequence represents the soybean raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
         Raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 31-34; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0eda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP849359-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gastrointestinal flora; soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Raffinose synthetase; metabolism modification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW57887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW57887 standard; Protein; 781 AA
                                Amino acid sequence of a raffinose synthase protein.
                                                      26-0CT-1999
                                                                            AAY30143;
                                                                                                 AAY30143 standard; Protein; 781
                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAV40801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SUMO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JUN-1998
                                                                                                                                                      758 edkmlrvqvpwp 769
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                                                                                                                                                                            ω
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                                                                                                                      7
                                                                                                                                                                   QDQMVVVQVPWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1998-324670/29.
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                                                                                                                                                                                                 Similarity 66.7
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMITOMO CHEM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wantanabe E;
                                                                                                                                                                                                                                                         781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                      (first
                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96JP-0338673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97EP-0122417.
                                                                                                                                                                            14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthetase
          plant;
                                                                                                                                                                                                           62.5%;
           sucrose;
                                                                                                                                                                                                           Score 50;
Pred. No.
                                                                                                                                                                                                ced. No. 1.6;
Mismatches
                                                                                                  ₹
           raffinose
                                                                                                                                                                                                                       19;
                                                                                                                                                                                                  ۳.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              food additive;
                                                                                                                                                                                                                       Length
                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                        781;
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RESULT
AAB49400
QУ
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                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                 Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a raffinose synthase protein. The sequence is isolated from plant material. The protein forms raffinose by complexing alpha(1 to 6)- D-galactosyl hydroxyl group of the 6C of D-glucose residue in sucrose molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 25-27; 40pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycine max.
                Example 6; Page 24-27; 36pp; English
                                  New soybean plant promoters useful for generating with desired properties \dot{\phantom{a}}
                                                                N-PSDB; AAC89523
                                                                                          Ishige F, Watanabe
                                                                                                                                30-APR-1999;
01-SEP-1999;
                                                                                                                                                          27-APR-2000; 2000EP-0108962
                                                                                                                                                                              02-NOV-2000
                                                                                                                                                                                              EP1048733-A2
                                                                                                                                                                                                                                  Plant promoter; transgenic plant; desired property.
                                                                                                                                                                                                                                                     Soybean raffinose synthase
                                                                                                                                                                                                                                                                         07-MAR-2001
                                                                                                                                                                                                                                                                                          AAB49400
                                                                                                                                                                                                                                                                                                             AAB49400 standard; Protein; 781
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New raffinose synthase gene – is prepared from a plant material
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAZ10002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-NOV-1997;
18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP11215984-A
                                                                                                           (SUMO ) SUMITOMO CHEM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                                       3 QDQMVVVQVPWP 14
:|:|: ||||||
758 edkmlrvqvpwp 769
                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 8; Conserv
                                                                                                                                                                                                                                                                                                                             œ
                                                                        2001-104537/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1999-511112/43
                                                                                                                                                                                                                                                                                                                                                                                                                                           781 AA;
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                               99JP-0124527.
99JP-0247211.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97JP-0329006.
96JP-0338673.
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                                                                                                                                                                                                                                                                                                                                                                                                       62.5%;
                                                                                          Oeda K;
                                                                                                                                                                                                                                                                                                                                                                                             ω,
                                                                                                                                                                                                                                                                                                                                                                                                      Score 50; D
Pred. No. 1.
                                                                                                                                                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       DB
1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                 20;
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                                                                                                                                                                                                                                                                                                                                                                                                               Length 781;
                                            transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                             0;
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present invention provides novel plant promoters which can

be used

in

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RESULT
AAG53157
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Best Local Similarity
Watches 8; Conserv
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                18-MAY-1999;
19-MAY-1999;
20-MAY-1999;
21-MAY-1999;
24-MAY-1999;
25-MAY-1999;
27-MAY-1999;
                                                                                                                                                                                                                                    25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
                                                                                 14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
                                                                                                                   06-MAY-
                                                                                                                                                          19-APR-
21-APR-
23-APR-
23-APR-
28-APR-
30-APR-
30-APR-
                                                                                                                                                                                                                    08-APR-
16-APR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the production of transgenic plants which express genes with desired properties.
                                                                                                                                           04-MAY-1999
05-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                     protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG53157 standard; Protein; 484 AA.
                                                                           14-MAY
                                                                                                          11-MAY
                                                                                                                                    06-MAY-
                                                                                                                                                                                                                                                                                                              25-FEB-2000;
                                                                                                                                                                                                                                                                                                                               06-SEP-2000
                                                                                                                                                                                                                                                                                                                                              EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana.
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99US-013248.
99US-013248.
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99US-013248.
99US-013248.
99US-0132487.
99US-0132487.
99US-013425.
99US-013421.
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99US-013421.
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99US-013421.
99US-0134376.
99US-0134941.
99US-0135124.
99US-0135125.
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99US-0135022.
99US-0136782.
99US-0136782.
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99US-0130510.
99US-0130891.
99US-0131449.
99US-0132048.
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99US-0128234.
99US-0128714.
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99US-0126785.
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s-0130077.
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66.7%;
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Pred. No.
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05-AUG-1999;	AUG	A)3-AUG-1999;)2-AUG-1999;)2-AUG-1999;	2-AUG-1999;	8-JUL-1999;	7-JUL-1999;	7-JUL-1999;	3-JUL-1999;	3-JUL-1999;	22-JUL-1999;	22-JUL-1999;	22-JUL-1999;	21-JUL-1999;	21-JUL-1999;	21-JUL-1999;	20-JUL-1999;	20-JUL-1999;	19-301-1999;	19-JUL-1999;	19-JUL-1999;	19-JUL-1999;	16-JUL-1999;	16-JUL-1999;	L4-JUL-1999; L5-JUL-1999;	13-JUL-1999;	12-JUL-1999;)8-JUL-1999;)9-JUL-1999;	06-JUL-1999;)2-JUL-1999;)1-JUL-1999;	30-JUN-1999;	Z Z	NDC	23-JUN-1999;	z :	.B-JUN-1999;	z	8-JUN-1999;	z	8-JUN-1999;	8-JUN-1999;	8-JUN-1999;	8-JUN-1999;	8-JUN-1999;	7-JUN-1999;	6-JUN-1999;	6-JUN-1999;	0-JUN-1999;	0-JUN-1999;	A-JUN-1999;	4-JUN-1999;	***************************************
990S-0147192	9908-0147302	99US-014/204	9905-0147038	99US-0146389	9905-0146386	9905-0145951	99US-0145918	990S-0145913	9905-0145224	99US-0145218	9905-0145192	9908-0145089	99US-0145087	9908-0145088	99US-0145086	9905-0144884	9908-0144632	9905-0144352	555770-51166	9908-0144333	99US-0144332	990S-0144325	9908-0144086	9905-0144085	990S-0143624 990S-0144005	9908-0143542	99US-0142977	990S-0142803	9908-0142390	99US-0142055	99US-0141842	99US-0141287	9905-0140823	99US-0140695	99US-0140354	9908-0139899	99US-0139817 99US-0139817	9908-0139750	9905-0139463	99US-0139461	9908-0139460	92765TO-5066	9908-0139457	9908-0139456	99US-0139454	99US-0139492	9908-0139453	9905-0139119	99US-0138847	9908-0138540	9908-0137724	990S-0137502.	,
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56.2%;		9US-016214	9US-016199	9US-016199	9US-016136	9US-0161360	9US-0161406	9US-016140	9US-0160989	9US-0160981	9US-0160815	908-016081	905-0160770	9US-0160767	9US-0160741	90S-0159638	9US-0159637	9US-0159331	905-0159330	9US-0159295	9US-0159294	908-0158369 908-0158369	9US-0158232	9US-0158029	9US-0157753 9US-0157865	9US-0157117	908-0156596	9US-0155659 9US-0156458	9US-0155486	9US-0154//9 9US-0155139	9US-0154039	9US-0154018	9US-0153070 9US-0153758	9US-0152363	905-0151438 905-0151930	908-0151303	9US-0151080 9US-0151080	9US-0151065	9US-0150884	9US-0149930	9US-0149902	9US-0149723 9US-0149723	905-0149722	9US-01491/5	9US-0149368 9US-0149368	9US-0148684	9US-0148565	905-0148319 905-0148319	9US-0148171	9US-014793	9US-0147416 9US-0147416	990S-0147303.	
Score 45;																																																					
DB 21																																																					
DB 21; Length 484;																																																					

RESULT 10 AGG3156 standard: Protein: 563 AA. AGG3156: XX XX AGG3156: XX AGG3156: XX AGG3156: XX XX AFABSI168: XX XX XX XX XX XX XX XX XX	Best Local Similarity 53.8%; Pred. No. 7.3; Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0; Qy 2 DQDQMVVVQVPWP 14 : :
אק יק	무 유 유 유 유 유 유 유 유 유 유 유 유 유 유 유 유 유 유 유
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Best Local
Matches
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20-AUG-1999
20-AUG-1999
20-AUG-1999
23-AUG-1999
23-AUG-1999
25-AUG-1999
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27-AUG-1999
31-AUG-1999
31-AUG-1999
31-AUG-1999
31-AUG-1999
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07-OCT-1999;
08-OCT-1999;
12-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
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29-SEP-1999;
04-OCT-1999;
05-OCT-1999;
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13-AUG-1999;
13-AUG-1999;
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23-SEP-1999;
24-SEP-1999;
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16-SEP-1999;
20-SEP-1999;
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18-OCT-1999;
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          536
                         N
         dedemlvgddpwp 548
                        DQDQMVVVQVPWP 14
                                        Similarity 53.6
7; Conservative
                                                                     99US-0161361.
99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
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99US-0161405.
99US-0161406.
99US-0161359.
99US-0161360.
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99US-0159637.
99US-0159638.
99US-0159584.
99US-0160741.
99US-0160767.
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99US-0158232.
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99US-0157753.
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990S-0154018.
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99US-0151080.
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99US-0149426.
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99US-0160770
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99US-0159330.
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99US-0151930
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99US-0150884.
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99US-0149902.
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99US-0148684
                                                                                                                                                      99US-0160989
                                                                                                                                                                                      99US-0160814.
                                               56.2%;
                                       Score 45; DB 21; Length 563; Pred. No. 8.7; 3; Mismatches 3; Indels
                                        0
                                       Gaps
                                        0
á
                Query Match
Best Local S
Matches 7
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RESULT 11
AAX32075
ID AAY320
XX AAY320
XX AAY320
XX AAY320
XX Fapese
XX Raffin
XX EP9536
XX EP9536
XX C1affin
XX Raffin
XX Raffin
XX Raffin
XX Raffin
XX Raffin
XX C1affin
                                  This sequence represents rapessed raffinose synthase, a protein that can bind a D-galactosyl group through an alpha(1-6) bond to the hydroxy group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. cDNA (see AAZ20210) encoding the enzyme was isolated from rapessed cv. Westar leaf cDNA by PCR. Probes or primers generated from plant raffinose synthase genes (see AAZ20207-10) may be used to obtain other raffinose synthase genes by labeled detection or amplification (claimed). These genes may be used to control the levels of raffinose produced in plants. Antisense genes can be used to knock out existing gene activity, and sense genes to increase the level of gene activity. The resulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacterla, corproviding general health advantages.
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30-APR-1998;
04-DEC-1998;
10-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-593144/51.
N-PSDB; AAZ20210.
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Misc-difference 143
                                                                                                                                                                                                                                                                                                                                                      Claim 27; Page 36-38; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            New sense and antisense genes, useful for altering the level raffinose in food plants \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Watanabe E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SUMO ) SUMITOMO CHEM CO LTD
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  Sequence
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  572
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98JP-0120551.
98JP-0345590.
98JP-0351246.
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144
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148
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                                                                                                                                                                                                                                                                                                                                                                                                                      of.
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Similarity 7; Conserv

Conservative

56.2%;

Score 45; DB Pred. No. 8.8; 3; Mismatches

20; <u>,</u>

Length 572; Indels

0

Gaps

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25-FEB-1999
05-MAR-1999
23-MAR-1999
25-MAR-1999
25-MAR-1999
25-MAR-1999
06-APR-1999
06-APR-1999
06-APR-1999
07-APR-1999
08-APR-1999
08-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
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23-APR-1999
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25-MAY-199
26-MAY-199
27-MAY-199
28-APR-199
29-APR-1999
28-APR-1999
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20-MAY-199
21-MAY-199
28-MAY-199
29-APR-199
   RESULT 1
AAG53155
ID AAG53155
AC AAG5
XX AAG5
XX AFAb
XX AFAb
XX Prot
KW Prot
KW Prot
KW Prot
KW Prot
KW Prot
XX Ep10
OS AFAb
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eesmvmvqvpw
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   990S-0121825.
990S-0125788.
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990S-012664.
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99US-0141287
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99US-0144332
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99US-0147303
99US-0148311
99US-0148311
99US-0148311
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RESULT 13
AAY32074
ID AAY320
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                                                        Query Match
Best Local Similarity 53.8
Matches 7; Conservative
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28-SEP-1999
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07-OCT-1999
07-OCT-1999
13-OCT-1999
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21-OCT-1999
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15-SEP-1999
16-SEP-1999
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22-SEP-1999
23-SEP-1999
                                                                                           26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
AAY32074 standard; Protein; 777 AA
                                 559
                                             N
                                dedemlygddpwp 571
                                            DQDQMVVVQVPWP 14
                                                                                                                                                                                                                                     990S-0154018
990S-0154018
990S-0154179
990S-0155139
990S-0155659
990S-0156458
990S-0156458
990S-0157753
990S-0157753
990S-0158029
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990S-0158039
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990S-0159638

990S-0160741

990S-0160767

990S-0160768

990S-0160981

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990S-01614084

990S-0161406

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990S-0161361

990S-0161361

990S-0161392

990S-0161992

990S-0161992

990S-0161993

990S-0161993
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99US-0149930.
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                                                                 56.2%;
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                                                                Score 45; DB 21; Pred. No. 9.1;
                                                           Mismatches
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                                                                       Length 586;
                                                           Indels
                                                           0
                                                           Gaps
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RESULT AAG07534
ID AAG
XX
AC AAG
XX
DT 17-0
XX
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Best Local Similarity
"~+~hes 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents mustard raffinose synthase, a protein characteristic that can bind a D-galactosyl group through an alpha(1-6) bond to the hydroxy group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. cDNA (see AAZ20209) encoding the enzyme was isolated from mustard (Brassica juncea) leaf cDNA by PCR. Probes or primers generated from plant raffinose synthase genes (see AAZ20207-10) may be used to obtain other raffinose synthase genes by labeled detection or amplification (claimed). These genes may be used to control the levels of raffinose produced in plants. Antisense genes can be used to knock out existing gene activity, and sense genes to increase the level of gene activity. The resulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacteria, or providing general health advantages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-APR-1998;
30-APR-1998;
04-DEC-1998;
10-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New sense and antisense genes, useful for altering the level raffinose in food plants - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers Misc-difference 210
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                    17-OCT-2000
                                                                 AAG07534;
                                                                                                       AAG07534 standard; Protein; 228
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 26; Page 29-31; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAZ20209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-593144/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Raffinose synthase; mustard; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JAN-2000
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754 eesmvmvqvpw 764
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                      (first entry)
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98JP-0120551.
98JP-0345590.
98JP-0351246.
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                                                                                                                                                                                                                                                                                                                         56.2%;
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                                                                                                                                                                                                                                                                                                                       DB
12;
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99US-0130077. 99US-0130149. 99US-0130510. 99US-0131449. 99US-0131449. 99US-0132484. 99US-0132486. 99US-0132486. 99US-0132486. 99US-0132486. 99US-0132486. 99US-0132486. 99US-0132486. 99US-0134218. 99US-0134219.

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RESULT 15
AAG45847
ID AAG458
XX
AC AAG458
XY
DT 18-OCT
XX
DT 18-OCT
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Arabid
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KW Protei
KW Protei
KW hybrid
KW termin
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OS Arabid
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Best Local S
Matches 8
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11-OCT-1999
12-OCT-1999
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31-AUG-1999;
01-SEP-1999;
07-SEP-1999;
10-SEP-1999;
13-SEP-1999;
                          Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                      18-OCT-2000 (first
 Arabidopsis thaliana.
                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 57609.
                                                                                           AAG45847;
                                                                                                           AAG45847 standard;
                    termination
                                                                                                                                                      2 DQDQMVVVQVPWP 14
| | | :| ||||
184 dgdwmlvgdvpwp 196
                                                                                                                                                                                        h 55.0%;
Similarity 61.5%;
8; Conservative
                    sequence.
                                                                                                                                                                                                                           9908-0154779
9908-0154386
9908-0155559
9908-0156596
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990S-0151930.
990S-0152363.
990S-0153758.
990S-0154018.
990S-0154018.
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3-0156596.
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S-0154779.
S-0155139.
                                                                       entry)
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                                                                                                            228
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4.8;
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23-MAR-1999
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99US-0123180.
99US-0123548.
99US-0125788.
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PR 01.JUL.1999 99US-0141842
PR 02.JUL.1999 99US-0142055
PR 08.JUL.1999 99US-0142059
PR 10.JUL.1999 99US-0142059
PR 11.JUL.1999 99US-0144065
PR 12.JUL.1999 99US-0144065
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PHICKMENT

auxin-Induced protein - Arabidopsis thaliana
c; Species: Arabidopsis thaliana (mouse-ear cress)
A; Varlety: columbia
C; Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 20-Jun-2000
C; Accession: H71407
C; Accession: H71407
R; Bevan, M; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.;
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.;
Avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk,
Nature 391, 485-488, 1998
A; Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Pulgdome
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; RESULT H71407 A; Molecule type: mRNA A; Residues: 1-164 <ABE> R; Theologis, A. submitted to the EMBL Data Library, December 1994 A; Reference number: \$71406 A; Accession: \$71408 auxin-induced protein IAA14 - Arabidopsis thaliana (fragment)

Nalternate names: indoleacetic acid-inducible protein IAA14

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 20-Aug-1999

C;Accession: S58501; S71408

R;Abel, S.; Nguyen, M.D.; Theologis, A.

J. Mol. Biol. 251, 533-549, 1995

A;Reference number: S58491; MUID:95387393

A;Accession: S58501 C.; Chalwatzis, N. A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis A;Reference number: A71400; MUID:98121113 A;Gene: IAA14 C;Superfamily: auxin-induced protein aux28 밁 ş A;Molecule type: DNA
A;Residues: 1-109,'S',111-164 <THE>
A;Cross_references: EMBL:U18416; NI A; Status: nucleic acid sequence not shown Query Match Best Local 9 Matches 120 DGDWMLVGDVPWP 132 2 DQDQMVVVQVPWP 14 Similarity 61.5%; 8; Conservation NID:g972930; PIDN:AAC49055.1; PID:g972931 Score 44; DB Pred. No. 1.6; Mismatches auxin-inducible mRNAs in Arabidopsis thai ? Length 164; 0, Gaps Pu1gdomen 0 S

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C; Genetics:
A; Map position:
C; Superfamily: &
A;Cross-reference
C;Genetics:
A;Gene: dl3315c
A;Map position: 4
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Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Ma Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; T ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A,7itle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: H86173
A;Accession: H86173
A;Status: preliminary
A, Maccession: Jeroc. Nan
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Status: DNA
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A;Cross-references: GB:Z97336; NID:g2244788; PIDN:CAB10234.1; PID:g2244811
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                                                                                                                                 A;Title: Sequence and analysis of chromosome 4 of A;Reference number: A85001; MUID:20083488 A;Accession: C85159 A;Status: preliminary
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C;Genetics:
A;Map position: 1
C;Superfamily: auxin-induced protein aux28
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A; Residues: 1-234 <STO>
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A; Residues: 1-229 <STO>
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C:Accession: C86467

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alor Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

N;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A;Authors: Hunter, J.L.; Jin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzis, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzis, R.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallcker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: C86467
                                                                                                                                                                                                                                                                                                                                    hypothetical protein F18021.60 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000 C;Accession: T47727 R;Benes, V; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Rudd, S.; submitted to the Protein Sequence Database, April 2000 A;Reference number: Z24474
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A; Introns: 244/2; 491/1;
A; Note: F18021.60
C; Superfamily: unassigned
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A;Molecule type: DNA
A;Residues: 1-719 <BEN>
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A;Molecule type: DNA
A;Residues: 1-619 <STO>
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A;Experimental source: cultivar Columbia;
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                        54.5%;
  Score 44; DB
Pred. No. 8.2;
4; Mismatches
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                      DB 2;
8.2;
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                                                                                                                                                                                                                     clone F1802
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                                            Length 719,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 619
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F;45-63/Product: VLDL receptor #status predicted <AXT>
F;45-68/Promain: extracellular #status predicted <EXT>
F;45-787/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;90-126/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;131-167/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;131-206/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;131-27/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;211-247/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;257-291/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;265-330/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F;336-337/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F;336-337/Domain: LDL receptor VWTD-containing repeat homology <LDL8>
F;459-498/Domain: LDL receptor YWTD-containing repeat homology <WW1>
F;499-544/Domain: LDL receptor YWTD-containing repeat homology <WW3>
F;584-587/Domain: LDL receptor YWTD-containing repeat homology <WW3>
F;584-587/Domain: LDL receptor YWTD-containing repeat homology <WW3>
F;632-674/Domain: LDL receptor YWTD-containing repeat homology <W%5>
F;675-717/Domain: LDL receptor YWTD-containing repeat homology <W%5>
F;726-769/Domain: LDL receptor YWTD-containing repeat homology <W%5>
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A; Residues: 1-863 x802
A; Cross-references: EMBL:X80207; NID:g609265; PIDN:CAA56505.1; PID:g609266
A; Cross-references: EMBL:X80207; NID:g609265; PIDN:CAA56505.1; PID:g609266
C; Comment: This receptor mediates uptake of very low density lipoprotein and vitellogen:
C; Comment: There is some evidence for the existence of a longer splice form containing a
C; Comment: There is some evidence for the existence of a longer splice form containing a
C; Superfamily: LDL receptor; Eff homology; LDL receptor ligand-binding repeat homology;
C; Keywords: duplication; fatty acid metabolism; glycoprotein; receptor; transmembrane pi
C; AdvDomain: signal sequence #status predicted cstars
E; 1-44/Domain: signal sequence #status predicted cstars
E; 1-45/E; 1-
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Plant Physiol. 123, 1087-1096, 2000
A;Title: Characterization of sulfate assimilation in A;Reference number: Z26003; MUID:20349720
A;Accession: T52251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Chicken oocyte growth is mediated by an eight ligand binding repeat member of A;Reference number: S51789; MUID:95045409
A;Accession: S51789
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A; Residues: 1-423 <GAO>
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#status predicted <TMM>
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Pred. No.
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R;Telford, E.A.; Watson, M.S.; Perry, J.; Cullinane, J. Gen. Virol. 79, 1197-1203, 1998
A;Title: The DNA sequence of equine herpesvirus-4. A;Reference number: Z22173; MUID:98264497
A;Accession: T42584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; De ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; A;Authors: Hunter, J.L.; Jin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; M. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; M. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                 tegument protein 40 - equine herpesvirus 4 (strain NS80567)
C;Species: equine herpesvirus 4
A;Variety: strain NS80567
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C;Accession: T42584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
""" 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
A;Map position:
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C; Superfamily: varicella-zoster virus gene 38
                                                                                                                       A; Molecule type: DNA
A; Residues: 1-529 <TEL>
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A;Molecule type: DNA
A;Residues: 1-500 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-200:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein AAD39294.1 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                       A;Cross-references: EMBL:AF030027; NID:g2605950; PIDN:AAC59558.1; PID:g2605986
A;Experimental source: strain NS80567
                                                                                                                                                                     A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE005172; NID:g5080784; PIDN:AAD39294.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: D86274
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Best Local
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5; Conserv
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35.7%;
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Pred.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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12;
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15;
protein
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R.; Marzia
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Query Match Best Local Similarity

52.5%;

Score Pred.

NO ;

DB 13;

Length 529;

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protein F1504.37 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: G86476
C;Accession: G86476
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference number: A86141; MUID:21016719
A;Accession: G86476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, S.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: C86468
A; Accession: C86468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-600 <STO>
A;Cross-references: GB:AE005172; NID:g10092376; PIDN:AAG12783.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable auxin response factor, 53188-50111 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) (C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
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                                                                                                                                                                                                                A; Cross-references:
                                                                                                                                                                                                                                          A; Residues: 1-767 <STO>
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                                                                                                                                                                                                                                                                                       A; Status: preliminary
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Best Local S
Matches 7
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               Best Local Similarity
Matches 6; Conserv
                                                                                                                                       position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 DQMVVVQVPWP 14
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               Conservative
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                                                                                                                                                                                                           GB:AE005172; NID:g8778363; PIDN:AAF79371.1; GSPDB:GN00141
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Pred. No.
                 5
                                        Score 42; DB
Pred. No. 20;
                      Mismatches
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15;
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                      Gaps
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probable IAA6 protein, 42631-41742 [imported] -
                           E96569
                                                                                                                        В
                                                                                                                                                                 Qy
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                                                  RESULT
                                                                                                                                                                                                                          Matches
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auxin-induced protein IAA6 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Decies: Arabidopsis thaliana (mouse-ear cress)
C;Date: 29-Nov-1995 #sequence_revision 01-Mar-1996 #text_change 20-Aug-1999
C;Accession: S58493
R;Abel, S; Nguyen, M.D.; Theologis, A.
J. Mol. Biol. 251, 533-549, 1995
A;Title: The PS-IAA4/5-like family of early auxin-inducible mRNAs in Arabidopsis thal A;Reference number: S58491; MUID:95387393
A;Accession: S58493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB: M86664; NID: 9330791; PIDN: AAB02476.1; PID: 9330833 R; Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J. Virology 189, 304-316, 1992 Virology 189, 304-316, 1992 A; Title: The DNA sequence of equine herpesvirus-1. A; Reference number: A41831; MUID: 92295566 A; Contents: annotation; possible protein coding frames A; Note: neither amino acid nor nucleotide sequence is given C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: The DNA sequence
A; Reference number: A36805
A; Accession: F36799
A; Molecule type: DNA
A; Residues: 1-530 <TEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: F36799
R;Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J. submitted to GenBank, March 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene 40 protein - equine herpesvirus 1 (strain Ab4p)
C;Species: equine herpesvirus 1
A;Note: host Equus caballus (domestic horse)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: 40
C;Superfamily: varicella-zoster virus gene 38 protein
                                                                                                                                                                                                                            C;Superfamily: auxin-induced protein aux28
C;Keywords: nucleus
                                                                                                                                                                                                                                                                             A; Gene: IAA6
                                                                                                                                                                                                                                                                                                                                 A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-189 <ABE>
                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: nucleic acid sequence not shown
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Best Local S
Matches 4
                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         621 EEDKMLVGEDPWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 DEIILIEEPWP 294
152 DRDWMLVGDVPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                              2 DQDQMVVVQVPW 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                              EMBL:U18408; NID:g972914; PIDN:AAC49047.1; PID:g972915
                                                                                                                            50.0%;
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36.4%;
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Pred. No.
                                                                                                                              Score 40; DB 2; Pred. No. 9.5;
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Arabidopsis thaliana

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C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Dates: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C.Accession: E39569
C.Hi, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Anthors: Hunter, J.C.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
A.; Authors: Money, T.; Rowley, D.; Sakano, H.
A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
Ker, W.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.; Reference number: A86141; MUID:21016719
A. Accession: E96569
A. Accession: E96569
A. Accession: Feferences: GB.AE005173; NID:96862944; PIDN:AAF30332.1; GSPDB:GN00141
C.; Genetics: Prelininary
A.; Map position: 1
C.; Superfamily: auxin-induced protein aux28
Ouery Match
Sest Local Similarity 58.3%; Pred. No. 9.5;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Ouery Match
Search completed: November 30, 2001, 09:41:43
Job time: 82 sec
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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AXI4_PAAU
AXI4_PAAU
AXI2_SOYBM
AXI2_ARATH
AXI6_ARATH
AXI6_ARATH
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Compugen Ltd.
P93830 arabidopsis
P98165 gallus gall
P28972 equine herp
038824 arabidopsis
Q55404 synechocyst
P16688 escherichia
Q52007 escherichia
P52007 escherichia
P52007 escherichia
P52007 escherichia
P52007 arabidopsis
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P49679 pisum sativ
P33077 arabidopsis
P49679 pisum secolus a
P13089 glycine max
P32294 phaseolus a
P32295 phaseolus a
P3267 arabidopsis
P30825 arabidopsis
P30825 arabidopsis
P30826 arabidopsis
P30827 xarabidopsis
P30827 xarabidopsis
P34027 xarabidopsis
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EMBL; U49073; AAB84354.1; -. EMBL; AC000104; AAB70451.2; -. EMBL; AF040631; AAC39439.1; -. Mendel; 7119; Arath; L524; 7119. InterPro; IPR003311; AUX_IAA.

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	a license agreement (See o license@isb-sib.ch).	modified and this statement is not removed	Institute. There	of Bioinformatics	wright It is	AUX/IAA FAM	(0)	AR /BY S	MEDIATING THE VARIOUS AUXIN-INDUCED EVENTS	EGULATOR OF GE	EMBL/GenBank/D	Ecker J.K.,	r K., Feng J	., Toriumi M.,			TOWN MINICACTORIS	rg P., Estelle	8901;			94:11786-117	A.; s among the Au	2315;		[1] SEOUENCE FROM N.A.		assicaceae; Ar	reptophyta; Em	ear cress).		PROTEIN IAA17 (INDOLEACETIC	equence update	ď)	PRT; 229 A		ALIGNMENTS	BP28_DROME PYY_MOUSE	BGAL_LACDE	ANDR_PANTR	ANDR_CANFA	ANDR_MOUSE	ANDR_PAPHA	ANDR_EULFC	LDVR_RABIT
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Best Local S
Matches 8
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"The receptor for yolk lipoprotein deposition in the chicken occyte.";

J. Biol. Chem. 266:18761-18770(1991).

-i- function: Binds vidl and vig transports them into cells by endocytosis. IN Order to be internalized, the receptor-ligand complexes must first cluster into clatherin-coated pits.

-i- Suscellular Location: Type I membrane protein.

-i- Tissue Specificity: Abundant in Occytes; much less in heart and
                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial
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P98165;

01-OCT-1996 (Rel. 34, Created)

01-OCT-1996 (Rel. 34, Last sequence update)

20-AUG-2001 (Rel. 40, Last annotation update)

VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR)

(VITELLOGENIN RECEPTOR) (VTG RECEPTOR).
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Multigene family; Nuclear
SEQUENCE 229 AA; 25288
   Pfam; P
PRINTS;
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=WHITE LEGHORN; TISSUE=Ovary;
MEDLINE=95045409; PubMed=7957081;
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                                                                                                                                                                                                         entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bujo H., Hermann M., Kaderli M.O., Jacobsen L., Sugawara Nimpf J., Yamamoto T., Schneider W.J.;
                                                                                                     InterPro;
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; IPR000152; Asx_hydroxy); IPR000561; EGF_11ke.
; IPR001881; EGF_Ca.
; IPR002172; LDL_recept_J; IPR00033; Ldl_reptor_J; O0057; ldl_recept_a; 8.
; PR00261; LDLRECEPTOR.
                                                                                                                                                                                         email to license@isb-sib.ch).
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EGF-like.
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PROSITE; PS00022; EGF 1; FALSE_NE
PROSITE; PS01186; EGF 2; 3.
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                LUL-RECEPTOR CLASS A 1.
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LUL-RECEPTOR CLASS A 6.
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LUL-RECEPTOR CLASS A 7.
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LUL-RECEPTOR CLASS B 5.
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EGG-LIKE 3.
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P28972;
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           STRAIN-CV. COLUMBIA; MEDLINE-95387393; PubMed-7658471;
                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
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"The DNA sequence of Annino"
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NCBI_TaxID=31520;
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                                   SEQUENCE FROM N.A.
                                                                                                                                   AUXIN-RESPONSIVE PROTEIN
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hes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e DNA sequence of equine herpesvirus-1.";
blogy 189:304-316(1992).
SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL21,
EHV-1 40, EHV-4 UL21, AND VZV 38.
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Nguyen M.D.,
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o RNA stage; Herpesviridae;
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Pred. No.
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Mendel; 7122; Arath;1524;7122.

InterPro; IPR003311; AUX_IAA.

Pfam; PF02309; AUX_IAA; 1.

Multigene family; Nuclear protein; Translation regulation.

MULTIGENE SEQUENCE 189 AA; 21017 MW; 5E9C1477A3877430 CRC64;
                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).

--- CATALTTIC ACTIVITY: ATP + ACETATE + COA = AMP + PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ACETYL-COENTYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL-ACTIVATING ENZYME).
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J. Mol. Biol. 251:533-549(1995).
J. FUNCTION: COULD ACT AS REGULATOR OF GENES RESPONDING THE VARIOUS AUXIN-INDUCED EVENTS RESPONDING (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
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Sugiura M., Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=96127529;
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30-MAY-2000
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                                                   EMBL; D64003;
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SIMILARITY: BELONGS TO THE AUX/IAA FAMILY.
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                                                   BAA10498.1; -
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A., Sato S., Kotani H.,
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01-AUG-1990
01-NOV-1991
20-AUG-2001
                                                                                                                                                                                                                      Chen C.-M., Ye Q.-Z., Zhu Z., Wanner B.L., Walsh C.T.;

"Molecular biology of carbon-phosphorus bond cleavage. Cloning a sequencing of the phn (psib) genes involved in alkylphosphonate uptake and C-P lyase activity in Escherichia coli B.";

J. Biol. Chem. 265:4461-4471(1990).

-i- FUNCTION: BELONGS TO AN OPERON INVOLVED IN ALKYLPHOSPHONATE UPTAKE AND C-P LYASE. EXACT FUNCTION NOT KNOWN.

-i- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF STRAIN K12.
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                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Makino K., Kim S.K., Shinagawa H., Amemura M., Nakata Molecular analysis of the cryptic and functional phn phosphonate use in Escherichia coli K-12."; J. Bacteriol. 173:2665-2672(1991).
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                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Burland V.D., Plunkett G. III, Sofia
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SEQUENCE FROM N.A
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Bacteria; Proteobacteria;
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PHNJ OR B4098.
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              EMBL; J05260
PIR; B35719;
                                                                                                                                                                                                                                                                                                                                   MEDLINE=90170953; PubMed=2155230;
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            J05260; AAA24348.1; -. B35719; B35719.
                                                      D90227; BAA14270.1; -. U14003; AAA96997.1; -.
                                         AE000482; AAC77059.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-K12 / MG1655;
MEDLINB-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., Rc
Gregor J., Davis N.W., Kirkpatrick H.A., Goe
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                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                             SEQUENCE OF 102-188 FROM N.A. STRAIN=K12 / MC4100;
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01-OCT_1996 (Rel. 34, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
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VARIANT 103 103 V -> L (IN STRAIN B)
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Bacteria; Proteobacteria; gamma subdivision;
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YECM OR B1875.
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Escherichia
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DYR2_HUMAN
Q92630;
Q92630;
P20-AUG-2001 (Rel. 40, Created)
P1-AUG-2001 (Rel. 40, Last sequence)
P1-AUG-2001 (Rel. 40, Last annotation)
P1-AUG-2001 (Rel. 40, Last annotation)
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             EMBL; Y13493; CAA738
EMBL; Y09216; CAA704
HSSP; Q16539; 1WFC.
MIM; 603496; -.
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CONFLICT
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                                                                                                                                                                                                                                                    Becker W., Joost H.-G.;
Submitted (NOV-1996) to
-1- FUNCTION: IN VITRO;
                                                                                                                                                                                                                                                                                                                               "Sequence characteristics, subcellular specificity of DYRK-related kinases, a specificity protein kinases.", J. Biol. Chem. 273:25893-25902(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DUAL-SPECIFICITY TYROSINE-PHOSPHORYLATION REGULATED KINASE
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                                                                                                                          the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Brain;
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                                                                                                                                                                                      MAILTED (NOV-1996) to the EMBL/GenBank/DDBJ databases. FUNCTION: IN VITRO; CAN PHOSPHORYLATE HISTONES H3 AND H2B ON AND THR RESIDUES. MAY BE INVOLVED IN THE REGULATION OF CELLUIG GROWTH AND/OR DEVELOPMENT.
SUBCELLULAR LOCATION: CYTOPLASMIC.
SUBCELLULAR LOCATION: CYTOPLASMIC.
STMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                              MNB/DYRK SUBFAMILY.
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CAA70418.1;
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3; Mismatches
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RESULT 9
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Matches 8
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BINDING
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                               Nakamura Y., Sakakibara J., Izumi T., Shibata A.,
"Transcriptional regulation of squalene epoxidase
inhibitors in HeLa Cells.",
J. Biol. Chem. 271:8053-8056(1996).
-I- FUNCTION: CATALYZES THE FIRST OXYGENATION STEI
BIOSYNTHESIS AND IS SUGGESTED TO BE ONE OF THE
ENZYMES IN THIS PATHMAY.
-I- CATALYTIC ACTIVITY: SQUALENE + AH(2) + O(2) -
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                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97432831; PubMed-9286711;
Nagai M., Sakakibara J., Wakui K., Fukushima
Tsuji S., Arakawa M., Ono T.;
"Localization of the squalene epoxidase gene
chromosome region 6q24.1.";
Genomics 44:141-143(1997).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;
ATP-binding; Phosphorylation.
DOMAIN
149
462
PROTEIN KINASE.
DOMAIN
155
163
ATP (BY SIMILARITY).
BINDING
178
178
ATP (BY SIMILARITY).
BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.
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Pfam; PF00069; pkinase; 2.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQLE OR ERG1.
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96215195; PubMed-8626488;
                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Liver
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                                                                                                                                                                  SUBUNIT: MAY FORM A COMPLEX WITH SQUALENE SYNTHASE.
SUBCELLULAR LOCATION: MICROSOMAL.
SIMILARITY: BELONGS TO THE SQUALENE MONOOXYGENASE FAMILY.
                                                                                                                                                                                                                     EPOXIDE + A + COFACTOR: FAD.
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8; Conserv
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Pred. No.
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ATP (BY SIMILARITY).
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; AF2C6822ED9522D7 CRC64;
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by ster
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D78130; D78129;

BAA22372.1; BAA11209.1;

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"hehes 6; Conserv
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SEQUENCE FRUM N....
STRAIN=CV, COLUMBIA;
STRAIN=CV, COLUMBIA;
MEDILINE=94105161; Pubmed=8278386;
MEDILINE=94105161; Pubmed=8278386;
Abel S., Oeller P.W., Theologis A.;
Abel S., Oeller P.W., Theologis A.;
*Early auxin-induced genes encode short-lived nuclear proteins.";
*Farly auxin-induced genes encode short-lived nuclear proteins.";
*Farly auxin-induced genes encode short-lived nuclear proteins.";
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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P49677; 023312;
01-FEB-1996 (Rel. 33, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
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IPR003042; Rng_mnoxgnase.
IPR000733; flavo_monooxygnse.
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E -> G (IN REF.
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Pred. No.
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RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
RA Nessenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
Schmabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Frishman D., Haase D., Lenck K., Mewes H.-W., Stocker S.,
RA Frishman D., Haase D., Lenck K., Mewes H.-W., Stocker S.,
RA Frishman D., Haase D., Lenck K., Huang E., Spiegel L.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Zachia P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Schnon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Schnon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Antonoiu B., Fulton E., Mardis E., Dante M., Pepin K., Hillier L.,
RA Antonoiu B., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Manner J., Fulton K., Strong C., Sun H., Lamar B., Yordan C.,
RA Manner J., Pereston R., Vil D., Shekher M., Matero A., Shah R.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McCombie W.R.;
Thalian "."
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Best Local
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                                                                               AXI2_ARATH STANDARD;
AXI2_ARATH STANDARD;
P49678; O22596;
O1-FEB-1996 (Rel. 33, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
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-!- FUNCTION: COULD ACT AS REGULATOR OF GENES |
MEDIATING THE VARIOUS AUXIN-INDUCED EVENTS
                                                                       IAA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thaliana.";
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota; Viridiplantae; Streptophyta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUXIN.
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58.3%;
Streptophyta; Embryophyta; Tracheophyta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB Pred. No. 13;
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AXI6 PEA
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P49680;
01-FEB-1996 (Rel. 33, La
01-FEB-1996 (Rel. 33, La
01-FEB-1996 (Rel. 33, La
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Best Local (
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STRAIN-CV. COLUMBIA;
MEDLINE-94105161; PubMed-8278386;
Abel S., Oeller P.W., Theologis A.;
Abel S., Oeller P.W., Theole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
STRAIN-CV. ALASKA;
MEDILINE-94016594; PubMed-8411182;
Oeller P.W., Keller J.A., Parks J.E., Silbert J.E., Theologis A.;
Oeller P.W., Keller J.A., Parks J.E., Silbert J.E., Theologis A.;
"Structural characterization of the early indoleacetic acid-inducible genes, PS-IAA4/5 and PS-IAA6, of pea (Pisum sativum L.).";
J. Mol. Biol. 233:789-798(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pisum sativum (Garden pea).
Eukaryota; Viridiplantae; Strep
Spermatophyta; Magnoliophyta; e
eurosids I; Fabales; Fabaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEA
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Mendel; 25258; Arath;1524;25258.
Interpro; IPR003311; AUX_IAA.
Pfam; PF02309; AUX_IAA; 1.
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-i- FUNCTION: COULD ACT AS REGULATOR OF GENES RESPONSIBLE FOR MEDIATING THE VARIOUS AUXIN-INDUCED EVENTS RESPONSIBLE FOR MEDIATING TH
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Malik M.K., Zimmerman J.L.;
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                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3888;
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SIMILARITY: BELONGS TO THE AUX/IAA FAMILY.
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Best Local S
Matches 7
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01-NOV-1995
                         between
the Euro
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                                                                                                                                                                                                                                         Conner T.W., Goekjian V.H., Lafayette P.R., Key J.L.; "Structure and expression of two auxin-inducible genes Arabidopsis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1993 (Rel. 27, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
AUXIN-RESPONSIVE PROTEIN IAA4 (INDOLEACETIC A
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Pfam; PF02309; AUX_IAA; 1.

Multigene family; Nuclear protein; Translation regulation.
SEQUENCE 179 AA; 20330 MW; 0D212F384D100D7E CRC64;
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SUBCELLULAR LOCATION: NUCLEAR
INDUCTION: BY AUXIN.
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                         ween the Swiss Institute of Bioinf European Bioinformatics Institute.
                                                                                                                                   INDUCTION: BY AUXIN.
SIMILARITY: BELONGS TO THE AUX/IAA FAMILY.
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                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                        GROWTH
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58.3%;
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Best Local Similarity
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EMBL; L15450; AAA16571.1; -.
PIR; S12243; S12243.
InterPro; IPR003311; AUX_IAA.
Pfam; PF02309; AUX_IAA; 1.
Multigene family; Nuclear protein; Translation regulation.
BEQUENCE 186 AA; 20975 MW; DCF66CAC4D28CD3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Hypocotyl;
Hashimoto H., Yamamoto K.T.;
"Three more members of the Aux/IAA gene family from mung bean (Vigna radiata) hypocotyl.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phaseolus aureus (Mung bean) (Vigna radiata).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
AUXIN-INDUCED PROTEIN 22C (INDOLE-3-ACETIC ACID INDUCED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                         EMBL; AB004931; BAA20847.1; --
Mendel; 25711; Phaau; 1524; 25711.
InterPro; IPR003311; AUX_IAA.
Pfam; PF02309; AUX_IAA; 1.
                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for content in the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARG12).
AUX22C OR ARG12.
                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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139
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FUNCTION: COULD ACT AS REGULATOR OF GENES RESPONSIBLE FOR MEDIATING THE VARIOUS AUXIN-INDUCED EVENTS RESPONSIBLE FOR CELL GROWTH (BY SIMILARITY).

SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

INDUCTION: BY AUXIN.
                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE AUX/IAA FAMILY.
DGDWMLVGDVPW 150
                            DQDQMVVVQVPW 13
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                                                                                                                                         PF02309;
NCE 188
                                                          Similarity
7; Conserv
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                                                            Conservative
                                                                                                                                    AUX_IAA; 1.
AA; 21273 MW; 1CF8A5842891329A CRC64;
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58.3%;
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RESULT 15

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oeller P.W., Keller J.A., Parks J.E., Silbert J.E., Theologis A.;
"Structural characterization of the early indoleacetic acid-inducible
genes, PS-TAA4/5 and PS-TAA6, of pea (Pisum sativum L.).";
J. Mol. Biol. 233:789-798(1993).
-i- FUNCTION: COULD ACT AS REGULATOR OF GENES RESPONSIBLE FOR
MEDIATING THE VARIOUS AUXIN-INDUCED EVENTS RESPONSIBLE FOR CELL
GROWTH (BY SIMILARITY).
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02309; AUX_IAA; 1.
Multigene family; Nuclear protein; Translation regulation SEQUENCE 189 AA; 21036 MW; BC699EF97443E580 CRC64;
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EMBL; X68216; CAA48298.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE AUX/IAA FAMILY.
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                                     November 30,
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58.3%;
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                                         2001, 09:40:56
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Pred. No.
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Mismatches
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Perfect score:
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Maximum Match 100%
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     4444444444444444
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1: sp_archea:*
2: sp_bacteria
3: sp_fung1:*
     100.0
61.2
55.0
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
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O9zt62 cucumis sat
O9fnd9 arabidopsis
O9lqe3 arabidopsis
O38832 arabidopsis
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O39c5w8 arabidopsis
O49162 arabidopsis
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O9xid8 arabidopsis
O90c8n7 arabidopsis
O9lqe8 arabidopsis
O9lqe8 arabidopsis
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O9lqe8 arabidopsis
O9c539 arabidopsis
O9c630 arabidopsis
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Q9M3I0	Q9UNR6	069545	Q9KSIB	Q9WHJ1	030731	Q9SHZ2	Q9R1M8	054929	Q9V6P0	Q9WRN9	P96217	Q9XE14	Q9PFC0	Q9FCE9	Q9нс65	Q9W433	Q9YGV9	Q9PY76	Q9PD55	Q9C2J0	Q92SY8	Q9XZD6	Q00629	Q9U194	019480
Q9m3i0 cicer ariet	Q9unr6 homo sapien	O69545 mycobacteri	Q9ks18 vibrio chol	Q9whj1 walleye epi	O30731 rhodobacter	Q9shz2 arabidopsis		O54929 mus musculu	Q9v6p0 drosophila	Q9wrn9 macaca mula	P96217 mycobacteri	Q9xe14 oryza sativ	Q9pfc0 xylella fas			Q9w433 drosophila	Q9ygv9 anguilla ja	Q9py76 human calic	Q9pd55 xylella fas	Q9c2j0 neurospora	Q9zsy8 arabidopsis	Q9xzd6 plasmodium	Q00629 manduca sex	Q9u194 leishmania	O19480 heterodontu

ALIGNMENTS

OS E DT	RESULT Q9FND9	DB Qy	X M O	SO	2 R R R R R	288888		RESULT Q9ZT62 ID Q
Q9FND9; 01-MAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) RAFFINOSE SYNTHASE PROTEIN. Arabidopsis thallana (Mouse-ear cress).	JUT 2 ND9 Q9FND9 PRELIMINARY; PRT; 783 AA.	1 YDQDQNVVVQVPWP 14 756 YDQDQNVVVQVPWP 769	Query Match 100.0%; Score 80; DB 10; Length 784; Best Local Similarity 100.0%; Pred. No. 9.4e-06; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	EMBL; AFU/3/44; AADUZ832.1; Transferase; Glycosyltransferase. SEQUENCE 784 AA; 86919 MW; 3B06A491F0908933 CRC64;	SEQUENCE FROM N.A. TISSUE-LEAF; Ohsumi C., Nozaki J., Kida T.; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.	Cucumis sativus (Cucumber). Cucumis sativus (Cucumber). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I, Cucurbitales; Cucurbitaceae; Cucumis. NCBI_TaxID-3659;	(9216); 01-MAY-1999 (TIEMBLIEL. 10, Created) 01-MAY-1999 (TIEMBLIEL. 10, Last sequence update) 01-MAY-2000 (TIEMBLIEL. 13, Last annotation update) RAFFINOSE SYNTHASE (EC 2.4.1.82).	162 162 092T62 PRELIMINARY; PRT; 784 AA.

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Q9LQE3;
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
                                                                                                                                                                                                 Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson (
Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam I
Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
Theologis A., Ecker J.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC007887; AAF79360.1; -.
InterPro; IPR003340; B3.
Pfam; PF02362; B3; 1.
SEQUENCE 570 AA; 65041 MW; E64A987BA713DF7E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structural analysis of Arabidopsis thaliana c
Sequence features of the regions of 1,044,062
physically assigned P1 clones.";
DNA Res. 4:291-300(1997).
EMBL; AB006702; BAB11595.1; -
SEQUENCE 783 AA; 86237 MM; 3C37D1D7871888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kotani H., Nakamura
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Ecker J.R.;
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DEDEMLVGDDPWP 570
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nilarity 72.7%;
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Q9C5W8;
01-JUN-2001
01-JUN-2001
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core ceurosids II; Brassicales; Brassicaceae; Arabidopsis
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J. Mol. Biol. 251:533-549(1995).

EMBL; U18416; AAC49055-1;

Mendel; 7130; Arath; 1524;7130.

InterPro; IPRO03311; AUX_IAA.
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Yamada K., Liu S.X., Sakano H., Pham P.K., Brooks S., Chao Q. Goldsmith A.D., Lee J.M., Toriumi M., Yu G., Brooks S., Chao Q. Chen H., Karlin-Neumann G., Kim C., Lam B., Miranda M., Nguyen Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R., Theologis A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                    "Full Length cDNA of gene d13315c/AT4g14550 (GI:7268161)."; submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF334718; AAG50096.1;
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                                                                                                                                                       InterPro; IPR003311; AUX_IAA. Pfam; PF02309; AUX_IAA; 1. SEQUENCE 228 AA; 25044 MW;
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STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
ROUSE D., Mackay P., Stirnberg P., Estelle M., Le;
"Changes in auxin response from mutations in an Ai
Science 279:1371-1373(1998).
EMBL; AF040632; AAC39440.1; -.
Mendel; 24578; Arath:1524;24578.
InterPro; IPR003311; AUX_IAA.
Pfam; PF02309; AUX_IAA; 1.
SEQUENCE 229 AA; 25304 MW; BDAA393475393545 C
                                                            EU Arabidopsis sequencing project; Submitted (MAR-2000) to the EMBL/C EMBL; 297336; CAB46059.1; -- EMBL; AL161539; CAB78497.1; -- EMBL; AL161539; Arath; 1524; 25847. InterPro; IPR003311; AUX_IAA.
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01-JUN-1998 (TrEMBLrel. 06, C.
01-JUN-1998 (TrEMBLrel. 06, L.
01-JUN-2001 (TrEMBLrel. 17, L.
IAA17/AXR3-1 PROTEIN.
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01-NOV-1999 (TIEMBLIEL 12, Last sequence update)
01-JUN-2001 (TIEMBLIEL 17, Last annotation updat
IAA7-LIKE PROTEIN (IAA7 LIKE PROTEIN).
DL3315C OR AT4G14550.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                  PF02309; AUX_IAA;
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Last annotation updat
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340A94E95B23FB60 CRC64;
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Q9LYN1; PRELIALL...

Q9LYN1; PREMBLERE1. 15, Created)

O1-OCT-2000 (TrEMBLERE1. 15, Last sequence update)

O1-JUN-2001 (TrEMBLERE1. 17, Last annotation update)

O1-JUN-2001 (TrEMBLERE1. 17, Last annotation update)

O-JUN-2001 (TrEMBLERE1. 17, Cress).
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O1-NOV-1999 (TrEMBLrel. 12, Created)
O1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
O1-NOV-1999 (TrEMBLrel. 17, Last annotation update)
O1-JUN-2001 (TREMBLREL. 17, Last sequence update)
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PIROTION update)

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;

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Vysotskala V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C.,
Vysotskala V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C.,
Lee J., Liu A., Li J., Kremenetskala I., Luros J., Gonzalez
Altafi H., Araujo R., Chao Q., Conn L., Conway A.B., Dunn P.
Hansen N., Huizar L., Kim C., Palm C., Rowley D., Shinn P.,
Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
"Arabidopsis thallana chromosome 1 BAC F23M19 sequence.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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Arabidopsis thaliana (Mouse-ear cress).
Brasyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidieurosids II; Brassicales; Brassicaceae; Arabidopsis.
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SEQUENCE FROM N.A. Benes V., Wurmbach
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B EU Arabidopsis sequencing project;

A EU Arabidopsis sequencing project;

B EMBL; AL163763; CAB87409.1; -.

R InterPro; IPRO00719; Euk_pkinase.

R InterPro; IPRO01519; LRR.

R InterPro; IPRO03592; LRR.out.

R Pfam; PF00560; LRR; 5.

R Pfam; PF00069; Pkinase; 2.

R Pfam; PF00069; LEURICHRPT.

R PRINTS; PR00019; LEURICHRPT.

R SMART; SM00370; LRR; 6.

R PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

R ATP-binding; Hypothetical protein; Transferase.

Q SEQUENCE 719 AA; 77329 MW; 3B91891A64E0DFD3 CRC64;
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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Q9X178
Q9X178;
01-NOV-1999
01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Gloning of 5'-adenyly1sulfate (APS) reductase from the macroalga Enteromorpha intestinalis.";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases EMBL; AR069951; AAC26855.1; -.
Mendel; 31988; Entin;1035;31988.

InterPro; IPR000063; Thiored.
InterPro; IPR002500; PAPS_reduct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              081350;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
5'-ADENYLYLSULFATE REDUCTASE (EC 1.8.99.).
Enteromorpha intestinalis (Hollow green seaweed).
Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae;
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Submitted (
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Pfam;
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SEQUENCE 423
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(TrEMBLrel.) (TrEMBLrel.)
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Pred. No.
Last sequence update)
Last annotation update)
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Pred. No.
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039281;
01-JAN-1998
01-JAN-1998
01-NOV-1998
COUNTERPART
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                             Telford E.A., Watson M.S., Perry J., Cullinane Submitted (OCT-1997) to the EMBL/GenBank/DDBJ dEMBL; AF030027; AAC59558.1; -. SEQUENCE 529 AA; 58150 MW; E2B737B89D489413
                                                                                                                                                                                                                                                                                        Nicolson L., Cullinane A.A., Onions D.E.;
"The nucleotide sequence of an equine herpesvirus
the herpes simplex virus 1 glycoprotein H gene.";
J. Gen. Virol. 71:0-0(0).
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                                                                                                                                                                                            MEDLINE=98264497; PubMed=9603335; Telford E.A.R., Watson M.S., Perry J., Cullinane Telford E.A.R., Watson M.S. Persvirus-4."; The DNA sequence of equine herpesvirus-4."; J. Gen. Virol. 79:1197-1203(1998).
                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses, no RNA stage;
Alphaherpesvirinae; Varicellovirus.
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(TIEMBLrel. 05, Last sequence update)
(TIEMBLEL. 08, Last annotation update)
OF HSV-1 GENE UL21 AND VZV GENE 38.
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RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Connu L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Chung M.K., Conn L., Conway A.B., Conway A.B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hospon C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetakaia I., Kurtz D.B., Kwan A., Liam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
Tegquence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
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EMBL; AC023913; AAG51894.1; -.

InterPro; IPR003311; AUX_IAA.

InterPro; IPR003340; B3.

Pfam; PF02309; AUX_IAA; 1.

Pfam; PF02362; B3; 1.

SEQUENCE 600 AA; 67933 MW; (
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Q9LQE8;
Q1-CCT-2000 (TrEMBLrel. 15, C:
Q1-CCT-2000 (TrEMBLrel. 15, L:
Q1-JUN-2001 (TrEMBLrel. 17, L:
F15Q4.37.
                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyte; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; educotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Q9C8N7;
Q9C8N7;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
AUXIN RESPONSE FACTOR, PUTATIVE.
                                                        SEQUENCE FROM N.A.
                                                                                                                    NCBI_TaxID=3702;
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(JUN-1999)
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A Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

A White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

A Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

A Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

A Chung M.K., Conn L., Conway A.B., Conway A.R., Fong B., Fujii C.Y.,

A Chung M.K., Conn L., Conway A.B., Conway C., Khan S., Fujii C.Y.,

A Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

A Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khan A., Lam B.,

A Hunter J.L., Jenkins J., Johnson-Hopson C., Khan A., Lam B.,

A Langin-Hooper S., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

A Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

A Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

A Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

A Lan G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

A Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Ra Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Ra Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Ra Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nayyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thouyeri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

--! SIMILARITY: TO GTP-BINDING ELONGATION FACTOR FAMILY.

EMBL; AC007887; AAF79371.1; -.

R InterPro; IPR000340; B3.

R InterPro; IPR000795; GTP_EFTU.

Ffam; PF02362; B3; 1.

R Pfam; PF02009; GTP_EFTU.

R GTP-binding: Protein biosynthesis.

SEQUENCE 767 AA; 85951 MW; FE29067F07D2E9F7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
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SEQUENCE FROM N.A.
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to the EMBL/GenBank/DDBJ databases
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RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT G., Fraser C.M., Venter J.C., Davis R.W.;
RT Haliana.";
RT Haliana.";
RL Nature 408.816-820(2000).
DR EMBL; AF336915; AAG53996.1; -.
DR EMBL; AF336915; AAG53996.1; -.
DR EMBL; AF336915; AAG53996.1; -.
DR EMBL; AC019018; AAG52268.1; -.
DR InterPro; IPR003311; AUX_IAA.
DR Pfam; PF02309; AUX_IAA; 1.
DR Pfam; PF02309; AUX_IAA; 1.
SQ SEQUENCE 189 AA; 21031 MM; 5E9B130584A75465 CRC64;
SEQUENCE 189 AA; 21031 MM; 5E9B130584A75465 CRC64;
SEQUENCE 189 AA; 21031 MM; 5E9B130584A75465 CRC64;
Sepurative 2; Mismatches 3; Indels 0; Gaps 0; Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Matches 7; Cons
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Database :
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Maximum Match 100%
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80
1 YDQDQMVVVQVPWP
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
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/cgn2_6/ptodata/2/1aa/backfiles1.pep:*
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US-08-846-234-3
US-08-846-234-5
US-08-846-234-5
US-08-935-484-2
US-09-350-484-2
US-09-964-922-5
US-09-964-922-5
US-09-964-922-5
US-09-491-362-7
US-09-491-362-2
US-09-491-362-2
US-09-491-362-2
US-09-491-362-2
US-09-491-355-2
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US-09-491-355-2
US-09-361-335-6
US-08-484-192-08-484-192-08-484-192-08-484-192-08-484-192-08-484-192-08-484-192-08-484-192-08-484-192-08-484-192-08-484-192-08-484-192-08-484-192-08-484-192-08-484-192-08-484-192-08-484-192-08-484-192-08-482-998-6
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US-08-431-333-6
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US-07-675-772-2
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	1 US-08-158-23-2-2 1 US-08-304-626-2 1 US-08-316-301A-2 2 US-08-611-928-2 2 US-08-611-928-2 3 US-09-173-891-2 4 US-09-076-137-2 5 PCT-US92-03624-2 6 5281530-1 6 5426049-1 1 US-08-447-411-45 2 US-08-662-227-2 4 US-09-017-947-2 2 US-08-662-227-35 4 US-09-230-637-61 1 US-08-396-550-1
	US-08-108-202-2 US-08-304-626-2 US-08-316-301A-2 US-08-611-928-2 US-09-173-891-2 US-09-173-891-2 US-09-076-137-2 PCT-US92-03624-2 5281530-1 5426049-1 US-08-662-227-2 US-09-017-947-2 US-08-662-227-35 US-09-017-947-3 US-08-662-237-35 US-09-017-947-3 US-08-662-237-35 US-08-276-967-2 US-08-276-967-2 US-08-276-967-2 US-08-276-50-1
US-08-158-232-2 US-08-304-626-2 US-08-316-301A-2 US-08-316-301A-2 US-08-316-301A-2 US-08-611-928-2 US-09-076-137-2 PCT-US-20-03624-2 5281530-1 US-08-462-227-2 US-08-662-227-2 US-08-662-227-35 US-08-08-276-2 US-08-276-2	-08-158-232-2 -08-304-626-2 -08-3104-626-2 -08-316-3114-2 -08-611-928-2 -09-173-891-2 -09-076-137-2 81530-1 -08-447-411-45 -08-662-227-2 -09-017-947-35 -09-017-947-35 -09-017-947-35 -09-037-61 -08-396-650-1
	Sequence

ALIGNMENTS

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RESULT 1
US-08-846-234-3
                                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ERAGMENT TYPE: internal
US-08-846-234-3
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                                                       Query Match
Best Local S
Matches 14
                                                                                                                                                                                                                                                  TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: OSUMI Chieko
APPLICANT: NOZAKI Jinshi
APPLICANT: KIDA Takao
TITLE OF INVENTION: RAFFINOSE SYNTHASE GENE,
TITLE OF INVENTION: PRODUCING RAFFINOSE, AND
                                                                                                                                                                                                                                                                                                                                TELEPHONE: (703)-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: OBLON
STREET: 1755 S.
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
                                                                                                                                                                                                                TYPE: amino acid TOPOLOGY: linear
1 YDQDQMVVVQVPWP 14
                                                                             Similarity
                                                       100.0%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                        24,618
                                                         0;
                                                                           Score 80; DB 4;
Pred. No. 4.4e-08;
                                                           Mismatches
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                                                                                             Length 14;
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RESULT 2
US-08-846-234-5
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                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08802466
Patent No. 5972606
GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (703)-413-2220
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 784 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: RAFFINOSE SYNTHASE GENE, METHOD FOR TITLE OF INVENTION: PRODUCING RAFFINOSE, AND TRANSGENIC PLANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: OSUMI Chieko
APPLICANT: NOZAKI Jinshi
APPLICANT: KIDA Takao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPETWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,466
                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                         APPLICANT: Creasy, et al.
TITLE OF INVENTION: HUMAN PROTEIN KINASE HOACF72
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         756 YDQDQMVVVQVPWP 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                           COUNTRY:
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100.0%; Pred. No. 4.9e-06;
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US-09-350-484-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09350484 Patent No. 6159716
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Creasy, et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: William T. Han
REGISTRATION NUMBER: 34,344
                                                                                          TELEX: <Unknown>
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19 Febru
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 610-270-4026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE:
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                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: William T. Han
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH50002
                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FASTSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,484
FILING DATE: 09-U1-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-4026
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19406
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTIÓN: HUMAN PROTEIN KINASE HOACF72
NUMBER OF SEQUENCES: 2
                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 528 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/802,466 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: PA
                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette
TOPOLOGY: linear
                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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66.7%;
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: MAKANISHI, Hiroyuki

APPLICANT: MAKANISHI, Hiroyuki

APPLICANT: MANDAI, Kenji

APPLICANT: MADA, MANABU

APPLICANT: OBAISHI, HIROShi

TITLE OF INVENTION: ACTIN FILAMENT-BINDING PROTEIN "L-AFADIN"

FILE REFERENCE: 98-1042*/LC(WMC)/653

CURRENT APPLICATION NUMBER: US/09/157,420

CURRENT FILING DATE: 1998-09-21

NUMBER OF SEQ ID NOS: 1

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO

LENGTH: 1829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-064-922-2
; Sequence 2, A
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; ORGANISM: rat
US-09-157-420-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-157-420-1
                         COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,922
FILING DATE: 22-APR-1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Applic
Patent No. 6180760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Callis, Judy
APPLICANT: Worley, Cathy K.
TITLE OF INVENTION: Sequences from Auxin-Induced Gene
TITLE OF INVENTION: Products Targeting Fusion Proteins for Degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               quence 2, Application US/09064922
tent No. 6222095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1246 QDRMAPVQNQWP 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 YDDDQGSYVQVP 141
TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 66.7%; tocal Similarity 66.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.7%; 65.
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CITY: San Francisco
STATE: California
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nes 7; Conserv
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .7e+02;
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-064-922-2
                                                                                                                  ; MOLECULE TYPE: US-09-064-922-5
                   Query Match
Best Local Similarity
"hes 7; Conservations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-064-922-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Applic
Patent No. 6222095
                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,922
FILING DATE: 22-APR-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hyman, Laurence J.
REGISTRATION NUMBER: 35,551
REGISTRATION NUMBER: 35,551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 46.2%;
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                   TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Callis, Judy
APPLICANT: Worley, Cathy K.
TITLE OF INVENTION: Sequence
TITLE OF INVENTION: Products
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 DGDWMLVGDVPW 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                    TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hyman, Laurenc REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 DODOMVVVQVPW 13
DQDQMVVVQVPW 13
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                                                                                                                                                   amino acid
GY: linear
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                                  Conservative
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                                                   46.2%;
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                                Score 37; DB Pred. No. 27; 1; Mismatches
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                                                                                                                                                                                                                                                                                     023070-085400US
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                                                                 Length 179;
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                                    Indels
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                                  0
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                                  Gaps
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135 DGDWMLVGDVPW 146

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RESULT 8
US-09-491-362-7
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TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-491-362-7
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APPLICANT: Croteau, Rodney B
APPLICANT: Lange, Bernd M
TITLE OF INVENTION: 1-DEOXY-D-XYLULOSE-5-PHOSPHATE REDUCTOISOMERASE, AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: WSUR14977
FILE REFERENCE: WSUR14977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09491362
Patent No. 6281017
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CURRENT FILING DATE: 2000-01-26
EARLIER APPLICATION NUMBER: 60/118,349
EARLIER FILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16,
                                                              APPLICATION NUMBER: US/08/764,870
FILING DATE: 13-DEC-1996
CLASSIFICATION: 530
PRIOR APPLICATION US 60/008,540
APPLICATION NUMBER: US 60/008,540
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                               COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NUCLEAR NAME OF TITLE OF INVENTION: Binding Domains
                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 QDSSVLAQLGWP 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                 STREET: Five Pai
CITY: Palo Alto
STATE: CA
                                  APPLICATION NUMBER: US 60/008,543 FILING DATE: 13-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 QDQMVVVQVPWP 14
 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
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milarity 50.0%;
Conservative
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Five Palo Alto Square,
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Baxter, John D
Fletterick, Robert J
Wagner, Richard L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apriletti, James W
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us 60/008,606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         3000 El Camino Real
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
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265 DOMAVIOYSW 274

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                                                                                                                       FEATURE:

NAME/KEY: DOMAIN

LOCATION: (184)..(437)

OTHER INFORMATION: minimal ligand binding domain

US-08-980-115-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-980-115-16
Q
                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/08/980,115
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: 08/764,870
EARLIER FILING DATE: 1996-12-13
EARLIER APPLICATION NUMBER: 60/008,606
EARLIER FILING DATE: 1995-12-14
EARLIER FILING DATE: 1995-12-13
EARLIER FILING DATE: 1995-12-13
EARLIER FILING DATE: 1995-12-13
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                                                                                                                                                                                                                                                                  SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 626662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 452 amino acids
                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Scanlan, Thomas S. APPLICANT: Baxter, John D. APPLICANT: Fletterick, Robert APPLICANT: Wagner, Richard L.
                                      Matches
                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: 60/008,540
EARLIER FILING DATE: 1995-12-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Shiau, Andrew K.
TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS FILE REFERENCE: UCAL-246/02US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: West, Brian L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kushner, Peter J.
APPLICANT: Apriletti, James W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Nakamura, Jackie N
REGISTRATION NUMBER: 35,966
REFERENCE/DOCKET NUMBER: UC/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)843-5000
                                                                                                                                                                                                                                 LENGTH: 45
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265 DQMAVIQYSW 274
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nes 6; Conserv
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 4 DQMVVVQVPW 13
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                                    Similarity 60.06; Conservative
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                                                          46.2%;
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Pred. No.
                                                            Score 37; DB Pred. No. 80;
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                                            Mismatches
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80;
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                                               Indels
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                                                 Gaps
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APPLICANT: Busch, Marco
APPLICANT: Hain, Rudiger
APPLICANT: Hain, Rudiger
APPLICANT: Hartin, William
APPLICANT: Tietjen, Klaus
APPLICANT: Kloti, Andreas
TITLE OF INVENTION: Method of determining the activity of
TITLE OF INVENTION: 1-deoxy-D-xylulose-5-phosphate reductoisomerase and
TITLE OF INVENTION: 1-deoxy-D-xylulose-5-phosphate synthase
FILE REFERENCE: 2020US
CURRENT APPLICATION NUMBER: US/09/449,335
CURRENT APPLICATION NUMBER: US/09/449,335
CURRENT FILING DATE: 1999-11-24
EARLIER FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO
LENGTH: 477
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-449-335-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: Croteau, Rodney B

APPLICANT: Lange, Bernd M

TITLE OF INVENTION: 1-DEOXY-D-XYLULOSE-5-PHOSPHATE REDUCTOISOMERASE, AND

TITLE OF INVENTION: METHODS OF USE

FILE REFERENCE: WSUR14977

CURRENT APPLICATION NUMBER: US/09/491,362

CURRENT FILING DATE: 2000-01-26

EARLIER FILING DATE: 60/118,349

EARLIER APPLICATION NUMBER: 60/118,349

EARLIER PILING DATE: 1999-02-03

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 475

TYPE: PRT
RESULT 13
US-09-449-335-6
; Sequence 6, Application US/09449335
; Patent No. 6303365
; GENERAL INFORMATION:
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Best Local Similarity
Watches 6; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Mentha piperita US-09-491-362-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-449-335-2
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                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09491362 Patent No. 6281017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                           332 QDSSVLAQLGWP 343
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Pred. No. 85;
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APPLICANT: Hain, Rudiger
APPLICANT: Martin, William
APPLICANT: Martin, Klaus
APPLICANT: Tietjen, Klaus
APPLICANT: Kloti, Andreas
TITLE OF INVENTION: Method of determining the activity of
TITLE OF INVENTION: 1-deoxy-D-xylulose-5-phosphate reductoisomerase and
TITLE OF INVENTION: 1-deoxy-D-xylulose-5-phosphate synthase
FILE REFERENCE: 2020US
CURRENT APPLICATION NUMBER: US/09/449,335
CURRENT FILING DATE: 1999-11-24
EARLIER APPLICATION NUMBER: DE 199 35 967.9
EARLIER FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 8
SOFTWARR: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LENGTH: 477
; TYPE: PRT
; ORGANISM: Arabidopsis thallana
US-09-449-335-6
; MOLECULE TYPE: US-09-041-886-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-09-041-886-11
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 6
                                                                                               TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Busch, Marco
                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Proapoptotic Peptides, Dependence TITLE OF INVENTION: Polypeptides and Methods of Use NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 QDSSVLAQLGWP 343
                                                             TYPE:
                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 4370 La
CITY: San Diego
                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                          amino acid
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4370 La Jolla Village Drive,
                                                                                918 amino acids
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                   protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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US-09-184-001-4

Sequence 4, Application US/09184001A
Patent No. 6303333

GENERAL INFORMATION:
APPLICANT: MICHALOVICH, DAVID
APPLICANT: SIMS, MATTHEW A.
APPLICANT: SIMS, MATTHEW A.
APPLICANT: SIMS, MATTHEW A.
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: US/09/184,001A
CURRENT FILING DATE: 1998-08-11
EARLIER APPLICATION NUMBER: 9817479.0
EARLIER FILING DATE: 1998-08-11
EARLIER APPLICATION NUMBER: 9806221.9
EARLIER FILING DATE: 1998-03-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ FOR Windows Version 3.0
SEQ ID NO 4
LENGTH: 400
TYPE: PRT
ORGANISM: HOMO SAPIENS
FEATURE:
INAME/KEY:
LOCATION: (53)(59)(98)
US-09-184-001-4
Search completed: November 30, 2001, 09:43:39 Job time: 198 sec
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US-09-184-001-4
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                                                                                                                                                                         Query Match 45.0%;
Best Local Similarity 35.7%;
Matches 5; Conservative
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||| |:| |
|731 DQMAVIQYSW 740
                                                                                              39 WSQGHCIVKLIPWP 52
                                                                                                                  1 YDQDQMVVVQVPWP 14
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Title:
Perfect score:
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Maximum |
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB seq length: 0
DB seq length: 2000000000
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2517
1 AAAAAACAACCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               November 30, 2001, 23:05:29; Search time 3540.92 Seconds (without alignments) 11726.727 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenEmbl:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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em_htgo_inv:*
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gb_sy:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1 E15707 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT		Result No. Sc 1 2 2 3 4 100 1 1 2 6 95 7 88 86 8 9 40 1 10 10 10 1 12 30 1 13 30 1 14 40 1 12 30 1 12 30 1 12 30 1 12 30 1 12 30 1 13 30 1 14 40 1 12 30 1 12 30 1 12 30 1 12 30 1 12 30 1 13 30 1 14 40 1 12 30 1 12 30 1 12 30 1 12 30 1 12 30 1 12 30 1 13 30 1 12 30 1 1
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2517 bp (tivus mRNA) (g1:5710390 973-A/1. ed. ed. lto 2517) 1 to 2517) 1 to 2517) 1 vozaki, J. SynTHASE G SyNTHASE G TO INC O		Length DB 2517 6 2569 8 2690 6 27467 6 1762 6 1762 6 27727 8 135295 8 2673 8 135295 8 120185 8 120185 8 120185 8 120185 8 120186 8 120185 8 120186
DNA PAT for raffinose synthase, c and Kida,T. and Kida,T. and Kida,T. (cucumber) /1 /1 /1 /1 /1 /1 /1 /1 /1 /1 /1 /1 /1	ALIGNMENTS	ID E15707 E25430 AF073744 E24424 E24423 E24425 E36418 E36426 E3796 E25448 AF007138 AF007138 AF007138 AF007148 AF
28-JUL-1999 complete cds. SE AND TRANSFORMED		Description E15707 Cucumis sat E25430 Raffinose s E36417 Raffinose s E36417 Raffinose s E24424 Raffinose s E24423 Raffinose s E24424 Raffinose s E24425 Raffinose s E36418 Raffinose s E36418 Raffinose s E36418 Raffinose s AJ311087 Pisum sat E30796 Raffinose s AJ00796 Raffinose s AL007913 Rabidops AL007913 Rabidops AC007913 Rabidops AC007913 Rabidops AC007913 Rabidops AL1513148 Persea am AC007913 Rabidops AC007913 Rabidops AL7271668 Cicer ari AF002451 Raffinose s AL7271668 Cicer ari AF003746 Oryza sat E25451 Raffinose s AL133248 Arabidops AL7475 Hordeum vul AC002328 Genomic s AL442104 Oryza sat E25451 C.arictinum AC008901 Homo sapi 166494 Sequence 14 AE006903 Sulfolobu AC027320 Homo sapi AC009956 Homo sapi AC009776 Homo sapi AC009776 Homo sapi AC00776 Homo sapi AC007776 Homo sapi AC007776 Homo sapi AC007776 Homo sapi AC007776 Homo sapi AC007774 Homo sapi AC007776 Homo sapi

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CC topology: Linear;
FH Key Location/Qualifiers
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FT CDS /product-'raffinose s
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E Chieko,O.J.N.N. and Kida.

Chieko,O.J.N.N. and Kida.

S Chieko,O.J.N.N. and Kida.

Raffinose synthase gene, process for producing raffinose transformed plant

L Patent: JP 199123080-A 1 11-MAY-1999;

AJINOMOTO CO INC

OS Cucumis sativus (Cucumber)

PN JP 1999123080-A/1

PD 11-MAY-1999

PF 24-OCT-1997 JP 1997292969

PF 24-OCT-1997 JP 1997292969

PF CHIEKO OZUMI,JINJI NOZAKI,TAKAO KIDA

PC C12N15/09,A01H5/00,C12N9/00/(C12N9/00,C12R1:19),C12

Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
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JP 1999123080-A/1.
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GYWGGLAPQVPCLPEARVIGVPLSPGLQMTMEDLAVDKIYLHKYGLYPPEKABEMYEG
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TVSPVTKLIQTSLHFAPTGLVINGLYTSGAIGSVGTSVDTDDLSSVBIGVKGCGEMRVFASK
KPRACRIDGEDVGFKYDQDQMVVVQVPWPIDSSSGGISVIEYLF"

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                                           unclassified.

1 (bases 1 to 2690)

Eijiro,W.K.O.O.

Raffinose synthase gene
Patent: JP 2000014389-A 1

SUMITOMO CHEM CO LTD

OS Brassica juncea
PN JP 2000014389-A/1
PD 18-JAN-2000

PF 10-DEC-1998 JP 19983

PR EIJIRO WATANABE,KENJ
PC C12N15/99,A01H5/00,C
(C12N1/21,C12R1:9),(C12N

(C12N9/88,C12R1:91),(C12N

FH KEY
CDS (134
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Raffinose syn
E36417.1 GI:
JP 2000014389
unidentified.
unidentified
                                     EIJIRO WATANABE, KENJI OEDA
C12N15/09, A01H5/00, C12N1/21, C12N5/10, C12N9/88, C12Q1/68//
12N1/21, C12R1:19), (C12N5/10, C12R1:91), (C12N9/88, C12R1:19), P
12N9/88, C12R1:91), C12N15/00, C12N5/00, C12R1:91) CC
Key Location/Qualifiers
CDS (134)...(2467).
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                                            TTAACATGCTAAACACTAGCGGTGCAATTCGATCCTTGGTGTATCATGAGGA-----AT
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AUTHORS Eljiro, W.K.O.O.

TITLE Raffinose synthase gene and use thereof
JOURNAL DY 199215984-A 2 10-AUG-1999;

SUMITOMO CHEM CO LTD

OS Glycine max(soybean)
PN JP 1999215984-A/2
PD 10-AUG-1999
PF 12-DEC-1997 JP 1997342899
PR 21JIRO WTANABE, KENJI OEDA
PC C12015/09,C07X14/415,C07X16/16,C12N1/21,C12N5/10,C12

C12015/00,C12R1:91),(C12N15/09,C12R1:91),(C12N1/21,C12N1/21,C12N1/21)
PC C12N15/00,C12R1:91),(C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/
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ACGCGTCGGAACCTGATAGCCGACATGTTGTTTTCGATTGGGAAGCTGAAGGATATTCGGT
                                                                            ACGCCAAGAGTAGTAAGAACAACGAGGACGACGTCGTTAGGTTGCTTCGTGGGCTTCC
                                                                                                                                                                          ACGGCCACCCTTTTCTCACGGAAGTTCCCGGAAAACATAATAGTCACCCCTTCACCCATCG
                                                                                                                                                                                                 ACGGTCATTCGTTCTGTCCGATGTTCCTGAGAACATTGTTGCTTCTCCCTTCTCCGTAC-
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JP 1999215984-A/2.
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/db_xref="taxon:32644"
521 c 673 g 65
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1400 1409	1 CATATTACAAAGCAATGACCAAATCAATAAATAAACATTTTAAAGGAAATGGAGTCATTG 	1341 1350
1340 1349	TTATCCACCTATTGGAGATGTTGTGTGAAGACTATGGAGGAGAGT	1281 1290
1280 1289	L TGTACGAAGGACTTCATGCTCATTTGGAAAAAGTTGGGATCGACGGTGTTAAGATTGACG 	1221 1230
1220 1229	L CGGTGGATAAGATTGTTCTTCATAAGGTCGGGCTGGTCCCGCCGGAGAAGGCTGAGGAGA 	1161 1170
1160	AGGCACGTGTGATTCAGCCAGTGCTTCACCAGGGCTGCAGATGACGATGGAGGATTTGG	1101
1100	TTTGGCATGCTTTGTGTGGATATTGGGGTGGCCTTCGCCCGCAGGTGCCTGGCTTGCCTG	1041 1050
1040 1049	GGATGAAGGCGTTTATAGATGAACTCAAAGGAGAGTTTAAGACTGTGGAGCATGTTTATG	981 990
989	ATTACAAATTCCGTGACGTCAATCCCAAGGCCACCGGCCCCGAGCCGGCCAGAAGG	921 945
920 944	GAATGAACCAAACCGTCGCCGGCGAGCAAATGCCCTGCCGTCTTTTGAAATTCCAAGAGA	861 885
860 884	TAATCGACGATGGTTGGCAATCCATCGGACACGATTCGGATCCCATCACCAAAGAAG	804 825
803 824	AGGGCGTAATAGAAGGCGTGAAGGCATCTCGTCGACGGCGGTTGTCCTCCCGGTTTAGTCC	744 765
743 764	GTATCGTGGACAAATTCGGTTGGTGCACGTGGGACGCGTTTTACCTAACGGTTCATCCAC	684 705
683 704	TGAAGATCGTGAGGACCCATCTTGGAACTTTTCGCTTGTTGGAGGAGAAGACTCCACCAG	624 645
623 644	TCCGAAGTATGTTGTATCTTCATGCTGGTGATCATCCGTTTGCACTTGTTAAAGAGGCGA	564 585
563 584	ATGATGACTTTGTCGATGTTTGTGTCGAGAGGTGGTTCGTCGAAAGTTGTTGATGCATCGT :	504 525
503 524	CGTATGTTTTCCTTCCGATCGTTGAGGGACCGTTCCGAACCTCGATTCAGCCTGGGG :	444
443 464	GGGATCTTGAATCGGAGACTCAGATTGTGATCACTTGAGAAGTCAGATTCTGGTCGAC (387 405
386 404	TTATGAGTATTTTCAGGTTTAAGGTTTGGTGGACTACACACTGGGTTGGTCGAAATGGTG :	327 345
344	ACGCGGACGAGCCCAGAAGCCGACACGTGGCTTCCCTGGGGAAGCTCAGAGGAATAAAAT	285

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6 E24423	CAATTGATTCTTCATCG	 GGGTAGTTGTAAAATTTGA	GGGAGGATGTTGGGTTCAAG	AAGGGTGTGGTGAGATGCG 	GTGGTGCCATTCAGTC	GTGGAGCCATCCA		AACTCATCCAAACT	ATCTTGACATAGCT	ATGTGTTTGCTGT	AAACCTTTGCGCTT	CGAGTCCTCAAGAC	CTAACCCAAAAGAC	GTCGTGAGACACGC	GAATCTCAA	GGAATCTCAACAAG	CCACACGAGACTGT	CGACTCGCGATTGT	TGCTCAAGAGCCTC	TTCTGAAAAAACTA	GGGCCATCTCTGGT	AGCCGGAI IGGGAC	ACCCTGACTGGGAT	TCCAAGGGTGTCAC	TCCAAGGATGTCAC	GCGTAGGAGATGAT	GTGTTGGTGATGAC	CAAGTATGGAACAT CGAGCATGGAGCAT	
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DNA		AGGATAAAATGCTG	AGGACC	CGAGTATTTGCATCGAAAAAKCAAGGGCTTGTCGTATTGATG 	TTGACAACCACATAGAT	TGGAGCCATCCAATCTGTGGACTATGACGATGACCTAAGCTCAGTCGAGATTGGTGTC	TCAAAAAAGTTAATTTGATTTGCTCCAATTGGATTAGTGAACATGCTTAACACTG	TTGCCCCAATTGGGCTG	TCTTGACATAGCTCTTGACCCATTCGAATTCGACCTCATCACTGTTTCACCAGTGACC. TCTTGACATAGCTCTTGGACCCATTCGACTCACTCACTGTTCACCAGTGACC.	TGTGTTTGCTGTATATTTGTTCAAGGACCACAAACTAAAGCTCATGAAGGCATCAGAG	CTTTGCGCTTTACCTCTATCAAGCCAAAAAACTTATCCTCTCCAAGCCCTCTCAAG	GCAATGGGAAAAGCCCAJ	CTAACCCAAAAGACATAGAATGGCACAGTGGAGAAAACCCCTATCTCTATTGAAGGCGTTA	GAGACACGCCGCAACCAATGCTTTTCACAATACTCAAAACGAGTGACATCCAAAA 	TTTTGGGTCTATTTAATT	AAGTTCACTGGAGTGATTGGTGCATTCAACTGCCAAGGAGGAGGATGGT		ACCCTTTGCATAATGGAC	TGCTCAAGAGCCTCGCTTTGCCTGATGGGACGATTTTGCGTTGTCAACACTATGCACTCC	ATGGATCGATCCTTCGA!	GAGCCATCTCTGGTGGACCAGTTTACGTTAGTGATTGTGTTGGAAAGCACAACTTCAA		ACCCTGACTGGGATATGTTCCAATCCACCCACCCTTTGTGCCGCCGTTCCATGCTGCCTGC	STECCTACAACAGCTTGT	CCAAGGATGTCACATTGTGCCAACGACAGCTTGTGGATGGGGAACTTCATCC	CGTAGGAGATGATTTTTGGTGCACTGATCCCTCTGGAGATCCAAATGGCACGTATTGGC	CGACCCCTCTGGTGATC	CAAGTATGGAACATTGTAACGACTTCATGTTCCTTGGCACGGAAGCTATCTCTTTGGTC	
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07-FEB-2		TTCCCTGGC	TGCCATGGC	GTATTGATG AACTAGATG	TTGGGGTTA	TTGGTGTCA	TTAACACTG	TTAACACTA	CAGTGACCA	CATCAGAGA	CCTCTCAAG	AAGGGATGA	AAGGCGTTA	CATCCAAAA CATGCTTAG	GTGGGTGGT	GAGGATGGT	TCAAAATTT	TTAAGATTT	ATGCACTCC	ATGCACTCC	 ACTTCAAGT	ACTTTGATC	CIGCCICIC	ATTTTATTC	ACTTCATCC	CGTATTGGC	CGTTTTGGC	CTCTTGGTC CCTTGGGC	
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DEFINITION
ACCESSION
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KEYWORDS
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AUTHORS
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Best Local Similarity 66.6%;
Matches 1421; Conservative
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AL Patent: JP 199215984-A 1 10-AUG-1999;
SUMITOMO CHEM CO LTD
OS VICIA faba(broad bean)
PN JP 199215984-A/1
PD 10-AUG-1999
PF 12-DEC-1997 JP 1997342899
PF 12-DEC-1997 JP 1997342899
PF 12-DEC-1997 JP 1997342899
PF C12N15/09,C07K14/415,C07K16/16,C12N1/21,C12N5/10,C12N9/88, PC
C12N15/09,C07K14/415,C07K16/16,C12N1/21,C12N1/21,C12N1/21,C12N1/21,C12N1/527,
PC C12N15/00,C12R1:91),(C12N9/88,C12R1:91),(C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527,C12N1/527
                                                    ACCTCGATTCAGCCTGGGGATGATGATCTTTGTCGATGTTTGTGTCGAGAGTGGTTCGTCG 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCAGATTC---TGGTCGACCGTATGTTTTCCTTCCGATCGTTGAGGGACCGTTCCGA 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGGTTGGTCGAAATGGTGGGGATCTTGAATCGGAGACTCAGATTGTGATCCTTGAGAAG 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGCTGAAGGATATTCGGTTTATGAGTATTTTCAGGTTTAAGGTTTTGGTGGACTACACAC 367
TACCTAACGGTTCATCCACAGGGCGTAATAGAAGGCGTGAGGCATCTCGTCGACGGCGGT 784
                                                                                                                                                                 AGTATACTAAAAGAAGCAGTTAAAGTAATCCAAACTCAGTTAGGAACATTCAAGACTCTT 778
                                                                                                                                                                                                                     GCACTTGTTAAAGAGGCGATGAAGATCGTGAGGACCCATCTTGGAACTTTTCGCTTGTTG 664
                                                                                                                                                                                                                                                                            AAAGTTGTTGATGCATCGTTCCGAAGTATGTTGTATCTTCATGCTGGTGATGATCCGTTT 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACGACTCCCTCGGACGACCCTATGTCTTACTCCTCCCAATCCTAGAAAACACCTTCCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTTGTTTCGTTGGTTTCAACTCCACCGAACCCAAAAGCCACCACGTAGTTCCACTCGGC 418
                                                                                                                                                                                                                                                                                                                                                                                          ACCTCACTCCAACCCGGTCTCAACGATCACATAGGCATGTCCGTCGAAAGCGGTTCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGGTCGGAACAAATGGACAGGAACTACAACACGAAACACAAATGTTAATCCTGGACAAA 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unclassified.
1 (bases 1 to 2746)
Eijiro, W.K.O.O.
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E24423
E24423.1 GI:13018163
JP 1999215984-A/1.
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/db_xref="taxon:32644"
552 c 621 g 79
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1. .2746
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Pred. No. 3.1e-266;
0; Mismatches 694;
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1864	ACTATGCTTAAGATTTGGAATCTCAACAAGTTCACTGGAGTGATTGGTGCATTCAACTGC	1805	Qy
1906	CAACATTACGCACTCCCTACAAGAGATTGCTTGTTTGAAGACCCTTTGCATAATGGCAAA	1847	ДĎ
1804	TACTATGCACTCCCGACTCGCGATTGTTTGTTTGAAGACCCTTTGCATAATGGAC	1745	Qy
1846	ANGCATAACITIGATCITCIGAAAAAKTAGIGCITCIGAIGGATCGAICCITCGAAGI	1787	pb Qq
78	CATGCCGCCTCACGAGCCATATCCGGCGGACCAATTTATGTTAGTGATTGTTTGG	.72) Db
68	- 8	1625	Qy
1726	ATGTTTC	1667	g
1624	TGGGGAACTTCATCCACCCTGACTGGGATATGTTCCAATCCACCCAC	Ġ	Qy
1666	ATGGTAC	1607	DЪ
1564	STACGTTTTGGCTCCAAGGATGTCACATGGTTCATTGTGCCAACGACAGCTTGTG		Qy
1606	GCCATATCCCTCGGCCGCGCGGGAGATGATTTTTGGTGCTCTGATCCATCTGGTGATCCA	1547	Db
1504	CTATCTCTCTTGGTCGTGTTGGTGATGACTTTTGGTGCACGGACCCCTCTGGTGATCC	1445	Qγ
1546	GGCAATGGTGTAATTGCTAGCATGGAGCATTGCAACGACTTCTTTCT	1487	Db
1444	GAAATGGAGTCATTGCAAGTATGGAACATTGTAACGACTTCATGTTCCTTGGCACGG	1385	Qy
1486	CTTATTACAAAGCACTAACCTCATCAGTGAAGAAA	1427	Db
1384	TGGATTTGGCAAAGGCATATTACAAAGCAATGACCAAATCAATAAATA	1325	Qy
1426	GTGTTAAAGTTGATGTTATCCATCTGCTTGAGTTACTATCAGAGGAATATGGTGGACG	1367	Db
1324	TTGACGTTATCCACCTATTGGAGATGTTGTGTGAAGACTATGGAGGG	N	Qy
1366	GATTTTGCACATGAGATGTTTGATGGGCTTCACTCTCATTTGGAGTCGGCGGGAATTGAC	1307	Db
1264	AGAAGGCTGAGGAGATGTACGAAGGACTTCATGCTCATTTGGAAAAAGTTGGGATCG	1205	Qy
1306	ACGATGGAGGATTTGGCGGTGGATAAGATTGTTGAGAACGGTGTGGGGCTAGTGCCGCCA	1247	Db
1204	CGATGGAGGATTTGGCGGTGGATAAGATTGTTCTTCATAAGGTCGGGCTGGTCCCCC	1145	Qy
1246	GTGCATGGGATGCCGAAAGCTAGGGTTGTTCCGAAGGTGTCTCAGGGGTTGAAGATG	1187	ДD
1144	TGCCTGGCTTGCCTGAGGCACGTGTGATTCAGCCAGTGCTTTCACCAGGGCTGCAGAT	1085	Qγ
1186	GTGGAGAGTGTTTATGTTTGGCATGCGCTTTGTGGGTATTGGGGCGGGGTTAGGCCTGGA	1127	Db
1084	GGAGCATGTTTATGTTTGGCATGCTTTGTGGGATATTGGGGTGGCCTTCGCC	1025	Qy
1126	GAGGGAAGAAAGGTTTGGGTGTTTTGTGAGGGATTTGAAGGAAG	1067	Db
1024	GCCAGAAGGGGATGAAGGCGTTTATAGATGAACTCAAAGGAGAGTTTAAGAC	965	Qy
1066	GTAAAATACGAAGAATTCTAAGTTTAGAGAATATGAGAATCCTGAA	1019	рb
964	GAAATTCCAAGAGAATTACAAATTCCGTGACTACGTCAATCCCAAGGCCACCGGCCCC	905	Qy
1018	GATGAAGATGATTCAGGAATGAACCGAACCTCAGCCGGGGAACAAATGCCATGCAGACTT	959	Дb
904	AGAAGGAATGAACCAAACCGTCGCCGGCGAGCAAATGCCCCTGCCGTCTT	845	Qγ
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844	GTCCTCCCGGTTTAGTCCTAATCGACGATGGTTGGCAATCCATCGGACACGATTCGGAT	785	ρ
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TITLE
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                       source
                                                              Eljiro, W. K. O. O.

Raffinose synthase gene and use thereof
Raffinose synthase gene and use thereof
Patent: JP 199215984 - A 3 10-AUG-1999;
SUMITOMO CHEM CO LTD
OS Stachlys Slaboldii(Chinese artichoke)
PN JP 199215984 - A/3
PN JP 1997342899
PR EIJIRO WTANABE, KENJI OEDA
PC C12N15/09,C07K14/415,C07K16/16,C12N1/21,C12N15/27,
PC C12N15/09,C07K14/415,C07K16/16,C12N1-21),(C12N15/10,C12N1-21),
PC C12N15/10,C12R1:91),(C12N15/99,C12R1:91),(C12N15/98,C12R1-91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),
PC C12N15/00,
PC C12N15/00,(C12N15/00,C12R1:91),(C12N5/00,C12R1:91),
PC C12N15/00,(C12N15/00,C12R1:91),(C12N5/00,C12R1:91),
PC C12N15/00,(C12N15/00,C12R1:91),(C12N15/90,C12R1:91),
PC C12N15/00,(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),
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PC C12N15/90,(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),
PC C12N15/90,(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),
PC C12N15/90,(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15/90,C12R1:91),(C12N15
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ON E36418 GI:13019216

E36418.1 GI:13019216

JP 2000014389-A/2.

Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Syermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

E 1 (bases 1 to 1762)

E 1 (bases 1 to 1762)

Raffinose synthase gene

L Patent: JP 2000014389-A 2 18-JAN-2000;
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OS Brassica napus

PN JP 2000014389-A/2

PD 18-JAN-2000

PF 10-DEC-1998 JP 1998351246

PR

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PC C12N15/09,A01H5/00,C12N1/21,C12N5/10,C12N9/88,C1201/68// PC

(C12N1/21,C12R1:19),C12N1/21,C12R1:91),C12R1:19), PC

(C12N1/21,C12R1:91),C12N15/00,C12R1:91),C12R1:19), PC

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                                                TTGACGATGCAAGATCTCGCCGTTGATAAGATCATCGATACCGGAATCGGATTCGTCTCG
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                                                            TTTATGTTTGGCATGCTTTGTGTGGATATTGGGGTGGCCTTCGCCCGCAGGTGCCTGGCT
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KSIVKNFNGNGHIASMQHCDDFFLGTKQISWFRVGDEMFQDPNGDPMGSFWLOGVH
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PIMQKFRGFPBCYKPIPGTHYTEVEWDQKEETSHLGKAEEYVYLNQAETH
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VKGGGSFLAYSSESPKKFQLNGCEVDFEWLGDGKLCVNVPWIEEACGVSDMEIFF"
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NLVLGGEQMSGRLHRFDECYKFRKYESGLLLGPNSPFYDPNNFTDLILKGIEHEKLRK
KREEAISSKSSDLAEIESKIKKVVKEIDDLFGGEQFSSGEKSEMKSEYGLKAFTKDLR
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                    TTAACACTAGTGGAGCCATCCAATCTGTGGACTATGACGATGACCTAAGCTCAGTCGAGA
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                                                                             CCGTTACAAA - - - GTTATGTGGCGGCATCAAATTTGCACCAATTGGGTTGACAAACATGT
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Stachyose synthesis in seeds of adzuki bean (Vigna angularis): molecular cloning and functional expression of stachyose synthe Plant J. 20 (5), 509-518 (1999)
20117502
2 (bases 1 to 3073)
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QAAAISAGGSDLAEIELMIVKVREEIDDLFGGKGKESNESGGCCKAAECGGNKDFTT
DLRTEFKGLDDVYWHALCGGWGGVPRGTTHLDSKIIPCKESPGLVGTMKDLAVDKIV
EGSIGLVHPHQANDLYDSMHSYLAQOTGVTGVKIDVIHSLEYVCEEYGGRVELAKAYYD
GLTNSIIKNENGSGIIASMQCNDFFFLGTKQIPFRVGDDFWFQDPNGDPMGVFWLQ
GYHMIHCSYNSLWMGQIIQPDWDMFQSSHECAKFHAGSRAICGGYVYVSDSVGSHDFD
LIKKLYFPDGTVPKCIYFPLPTRDCLFRNPLFDQKTVLKINNFNKYGGVIGAFNCQGA
GMDDKGKKFKGFPECYKAISCTVHVTEVEWDQKKEAEHHGKAEEYVVLNQAEVLHLM
TPVSEFLQLTIQPSTFELYNFVPVEKLGSSNIKFAPIGLTNWFNSGGTIQELFYIEKD
                                                                                                                                                                                                                                                                                                                                                       /product="galactinol-raffinose galactosyltransferase"
/protein_id="CAB64363.1"
/protein_id="CAB64363.1"
/db_xref="Gi:6634701"
/translation="MAPPNDPVNATLGLEPSEKVFDLSDGKLTVKGVVLLSHVPENVT
/ESSESSICVPRDAPSSILQRVTNASHKGGFLGFSHVSPSDRLINSLGSFRGRNFLSF
REXTMMSTQWVGNSGSDLQMETQWILLIEVPETESYVVIIPIIEKSFRSALHPGSDDHV
KICAESGSTQWVGNSGSDLQMETQWILLIEVPETESYVVIIPIIEKSFRSALHPGSDDHV
KICAESGSTQWVGNSSFGALAYVHVAETPYNLMREAYSALRVHLDSFRLLEEKTVPRIV
KICAESGSTQVVARASTFCVIIPIGGWGFMGLKDFSGGGVARRFVVIDDGGNSVNFDDEDFNEDAK
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/db_xref="taxon:3914"
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                                                                                                                                                                                                                                  Submitted (19-FEB-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7460)
On Jul 24, 2001 this sequence version replaced gi:13027312.
The orientation of the sequence is from T7 to SP6 of the PAC clone Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sasaki,T., Matsumoto,T. and Yamamoto,K. oryza sativa nipponbare(GA3) genomic DNA, clone:P0583G08
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Oryza sativa genomic DNA, chromosome 1,
complete sequence
AP003282
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1 (bases 1 to 135295)
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/chromosome="1"
/clone="p0583G08"
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                    14.5%;
                      Score 364; DB 8;
Pred. No. 1.1e-93;
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                                                                  TTGGCATGCTTTGTGGATATTGGGGTGCCCTTCGCCCGCAGGTGCCTGGCTTGCCTGA 1101
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                                                                                                              CATGGGCGGCTTCGTGAGGGAGATGAAGGCGGCGTTCCCGACGGTGGAGCAGGTGTACGT
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Matches 486; Conserv
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L Patent: JP 199313677-A 1 16-NOV-1999;

SUMITONO CHEM CO LTD

OS Unidentified

PN JP 199313677-A/1

PD 16-NOV-1999

PD 16-NOV-1998 JP 1998120550

PF 30-APR-1998 JP 1998120550

PR EIJIRO WATANABE, KENJI OEDA

PC C12N15/09,A01H5/00,C12N1/21,C12N5/10,C12N9/88,C12R1:19), (C12N9/88,C12R1:19), (C12N9/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATCCATGTA
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CCAATCCACCCTTGTGTGCCCCTTCCATGCTGCCTCTGGAGCCATCTCTGGTGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATCCACCTA 1291
                                                                                     GATCTATGTTAGTGATTCTGTGGGAAAGCATAACTTTGATCTTCTGAAAAAAACTAGTGCT 1719
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Raffinose synthetase go
E30796 1 GI:13017232
JP 1999313677-A/1.
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CC Topology: Linear;
FH Key LA
FT peptide 2
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Eijiro, W.K.O.O.
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E25448.1 GI:13024744
JP 1999123080-A/19.
Glycine max.
Glycine max
                                                                                                                                                                                          Patent: JP 19912:
AJINOMOTO CO INC
OS Glycine max (
PN JP 19912308
PD 11-MAY-1999
PF 24-OCT-1997;
PR CHIEKO OZUMI,
PC C12N15/09,A01
                                                                                                                                  Strandedness: I
CC Topology: I
FH Key
FT CDS
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Raffinose synthase gene,
transformed plant.
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                                                                                                                                                                                                                                                                                                              transformed plant
Patent: JP 1999123080-A 19
                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 2780)
Chieko, O.J.N.N. and Kida.
                                                                                                                                                                                                                                                                                                                                            Raffinose synthase gene,
                                                           751
                                                                                                                                                                             CHIEKO OZUMI,JINJI NOZAKI,TAKAO KIDA
C12N15/09,A01H5/00,C12N9/00//(C12N9/00,C12R1:19),C12N15/00
andedness: Double;
                                                                                                                                                                                                                                                                   Glycine max (Soybean)
JP 1999123080-A/19
                                                                                                                                                               Topology: Linear;
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                                                       /organism="Glycine max"
/db_xref="taxon:3847"
540 c 688 g 8
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156. .2405.
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Arabidopsis thallana g
AB006702 BA000015
AB006702.1 GI:2351067
Nakamura,Y.

Direct Submission
Direct Submission
Submitted (22-AUG-1997) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)
Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please
                                                                                                                                                                                    Sequence features of the regions of 1,044,062 thirteen physically assigned Pl clones DNA Res. 4 (4), 291-300 (1997)
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FEATURES
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clone is MSN9 and the 3' clone is K21I16.
Location/Qualifiers
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similar to unbra
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                           /translation="MQKKEEEDDSTVYGFTFLAEKLRVYVFSEKITGLRFWRENHRFS
FLAEKSRVFVFSGKITGLRFWRENHGFSFLAEKSRVFVFDWKITCFSFLAGKSRVYVF
GEKITGFCFWLENYWFFVFGGKITGFRFWRENHGFSFLAGKSRVFVFDGKIMVFIFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MDTCRNKCGGCYRQFNKKEHLVEHMRISYHSVHEPTCGICNKHC RSFDSLREHLIGPLFKQECKNIFSIRGCFFCLFILESPNARRIHGERCQLSNVTSGLM IRMAALGLRNKSTIDYTSSRBPRVALSCKMYGGGSDGSLDLCARVCITDESENVFH TYVKPTIPVTNYRYEMTGIRPENLRDAMRLKHAQRKVQEFLCNGEPMKIRPRNGKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MEELEKTOKFOKKKKQQQEKQDQSSPINFEMSSRSSLHSLPQTT
IESPPDSPTLSSIPDSHGSSPHTIIFTSVAKTETPFRVTNGEEKKVSESRROLRPS
FSSSSSTPRESKWASLIRKALLGFRUIAFVSCLVSFSVMVSDRDKGWAHDSFYNYKEF
RFCLAANVIGFVYSGFMICDLVYLLSTSIRRSRHNLRHFLEFGLDQMLAYLLASASTS
                                                                                                                                                                                                                                                                                                                                                                                                                            ILVGHGLDNHLDSLQLEYSSSMIRDTAEYPPLMKSSKLSNSLKYLTQAYLGYDIHVGI
QDPYEDCVATMRLYTRMRYQKHRAEAYPLASDTQNHNNFAAWRQNELERMSPEELLDL
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7039. .7169,7253. .7418))
                                                                                                                         /evidence=not_experimental
/protein_id="BAB11586.1"
/db_xref="GI:10178141"
                                                                                                                                                                                                                                                          similar to unknown protein'
                                                                                                                                                                                                                                                                                                                                                                                              SRSDYYCWCLDSVA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="exonuclease-like protein"
/protein_id="BAB11585.1"
/db_xref="GI:10178140"
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/note="gene_id:MPO12.
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/protein_id="BAB11584.1"
/db_xref="GI:10178139"
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NITGLRELRKNQGETELAGKSRVYVEWWKNYEETESQEIACIEKKEGKILILLDWERC
                                                                                                                                                                                                                           /codon_start=1
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join(2380. .2861.3626. .3761,4109. .4303)
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/strain="Columbia"
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TVSFSGILELEILKRKVSAFYBSNRGYGLTEYHEFGSYPGLEDKNNNDDDDDEEKNVN
DGLQWRAKRSRVEEVAALDHEESSSLQRSLEKCSGFPDHRLPHRRKEKSITEIIEKES
AAKVREETEPADGDVKSNVKSGRKKTKRHDEVUGDLENVTTTALWRRRKSEVATIEDG
GNKQVVESSKGKTSRKKKMDVDDGDDDGSGDKEESEEKEISDLEINIDSTSLASLRK
KVRFDDSVVERSTENGETATOTSKREKKKKLSESKVLSPDFLDFSRGRKKSTIESESSKV
SSGSQVDERVTDASDSLAMEVEEDTLDKPCEPSSDNGLGQEELSRELSNAUPFLRLGSYDSSDKEK
SSGSQVDERVTDASDSLAMEVEEDTLDKPCEPSSDNGLGQEELSRELSNAUPFLRLGSYDSSDKEK
SGELSENGKPVTNGKEEKDKKGKKGKKGKAKGKAEIETTGKEENBACHKKEEKKKKSESK
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DCDYVLDFECATLPFTYRYKYDRHPLKLCYDGDKDMAGSYWCEICEKEMDQNIIFYTC
ESSGPTIHIECYLGDFRYVKPRLHFEENKKWEVALNGINRPGYKCGFRCKGPFVAV
SVDYDISYYCSLLCLWKGETLVYGSIRD*
JOIN 19451. 19583,19713. 19842,20674. .21070)
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/protein_id="BAB11587.1"
/db_xref="GI:10178142"
/translation="MYLVEELSDVSSPTNEANQAYSYDDDDDDDSSLTPSMVFDQIMG
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PSHQRHPLMLLTHGLPQEAEDDKCRLCGEKVGKLVYHCSICDFSLDLFCARNDLSLVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="gene_id:MPO12.6 unknown protein"
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GLKRCGKSCRLRwmnyLSPnvnrgnftdqeedliirlhkllgnrwsliakrvpgrtdn
QVKNYWnThLSKKLGLGDHSTAVKAACGVESPPSMALITTISSSHQEISGGKNSTLRF
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EHRISRTYFLGSGDWKCGVCRRRMDGRYGAYSCSICPDYAVHSRCATRRDVWDGLELE
DEPEDLEECEEPFRVVSDGVINHFSHREHDLRLEDGLINRHDENIRCBACVRPVYANT
FYSCWQCDDFILHETCANLPRKKHVLHNHQLILYPDDNIVMDFPMLRGVFLCTACRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="Myb-related protein"
/protein_id="BAB11588.1"
/db_xref="GI:10178143"
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/db_xref="GI:10178144"
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gene_id:MPO12.5"
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/codon_start=1
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TTSYQHASNINQQLNYGNYVPESGSIMMPLSVDQSEQNYWSVDDLWPMNIYNGN"
join(37074. .37321,37502. .37628,37729. .38181)
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LAKSAGLKRTGKSCRLRWLNYLRPDVRRGNITPEEQLTIMELHAKWGNRWSKIAKHLP
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/protein_id="BAB11590.1"
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                                                                                                                                                                                                                                                                                                                                                            gene_id:MPO12.7"
                                                                                                                                                                                                                                                                                                                                                                                  complement(join(30305. .30671,31473./note="gb|AAD53092.1
                                                                                                                                                                                                                                                                                                                                                                                                                                        KLLLDGCEGGMTEEVKVKLEGEMVNLLEKVIEMRSS"
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DGEKAFESSLEKCPFTSNSTVKFRLKYPNERTEEKKTEAEVAETTMEVEYLKKKLDEM
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gene_id:MPO12.8"
                                 factor
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                                                        note="contains similarity to Myb-related transcription"
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                   CATTGTAACGACTTCATGTTCCTTGGCACGGAAGCTATCTCTCTTGGTCGTG---
                                                                                             GCAATGACCAAATCAATAAATAAACATITTAAAGGAAATGGAGTCATTGCAAGTATGGAA 1411
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NIYKNHWAATKRRLHSVRTKRSDAFSPRNNALLENYIRSITINNNALMNREVDSITANS
EIDSTRCENIVDEVMLINTHATTSVYVPEQAVLTWGYDFTKCYEPMDDTWMLMNGWN''
Complement(join(39428. .39519,39638. .39736,40283. .40371,
40599. .40654))
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46037. .46181,46269. .46640)
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Brassica oleracea
                                                                                                                                                      Direct Submission
Submitted (17-MAY-1994) Y. Fujikura, Dept of Plant Physiology,
Agriculture University, Arboretumlaan 4, 6703 BD Wageningen,
NETHERLANDS
                                                                                                                                                                                           Fujikura,Y.
Direct Subm
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2 (bases 1
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Fujikura,Y. and Karssen,C.K.
Cauliflower cDNA encoding a
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X79330
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                                                                                        /db_xref="taxon:3712"
                                                                                                                                         ocation/Qualifiers
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VTDEKPELSSSVVYSENRSPTALISLGVRGCGRFGAYSSQRPLRCAVDGTETEFNYDA
EVGLVTJALLPVTRSEMFFRNVEILV"
683 a 577 c 655 g 754 t
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282 ATAGCCGACATGTTGCTTTCGATTGGGAAGCTGAAGGATATTTCGGTTTTATGAGTATTTTCA 341
CAAAATTTCAAAAGAATG - - - ATCCTAAGGACACGCAAGTGTCAGGGCCTTAAGAGTG - - -
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                                                                                                                                      TGAACCAAACCGTCGCCGGCGAGCAAATGCCCCTGCCGTCTTTTGAAATTCCAAGAGAATT 923
                                                                                                                                                                                          TCATAGATGACGGTTGGCAACAAATAGAAAACAAAGAG------AAAGATTCAA
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                                                                                              ACTGCCTTGTCCAGGAAGGAGCACAGTTTGCTACTAGGCTTGTTGGTATAAAGGAGAACG
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                                           TCCCGACTCGCGATTGTTTGTTTGAAGACCCTTTGCATAATGGAGAAACTATGCTTAAGA 1817
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Search completed: December 1, 2001, 02:27:36 Job time: 12127 sec

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Result
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3: /SIDS2/gcgdata/geneseq/geneseqn/NA1982.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Soybean raffinose
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26-APR-1996;
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Yeast AOD9604-asso	AAH24065	22	4590			5
Oligonucleotide Dl	AAF58238		244	1.5	38.8	4
Human thioredoxin	AAA53450		66566		9	w
Human cDNA sequenc	AAH18536		3408		9	N
	AAA75403		1631			_
plant	AAH87795		540	٠	<u>∞</u>	0
Peppermint plant o	AAH87794		636			φ
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Oligonucleotide D2	AAF58262		936		7.	7
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	AAF58259		936	3.1		0
	AAF58257		936	3.1	78	ø
	AAF58254		936	3.1	78	80
Oligonucleotide D1	AAF58252		936	3.1	78	7
ntha	AAX61259		253	3.6	90.8	σ
Arabidopsis thalia	AAC42001		822		114	G
	AAZ10004		993			4
finos	AAV40803		993		169.6	w
raffinose	AAD00331		1816	6.9	174.4	N
raffinose s	AAD00333		3060		184	_
raffinose	AAD00337		2668		191.8	0
t raffinos	AAD00338		2653		220.8	9
raffinose	AAD00334		2842		240.8	æ
Corn raffinose syn	AAD00332		2868		243.2	7
	AAX61239		2780		275.8	σ
	AAZ20207	20	928	•	303.8	5
raf	AAZ20210	20	1762	•	868.4	4
œ	AAZ10003	20	1762	35.2	886.8	ω
Japanese artichoke	AAV40802	19	1762	•	886.8	N

ALIGNMENTS

Cucumber raffinose synthase cDNA. WPI; 1998-264858/24. P-PSDB; AAW53570. Cucumber; raffinose synthase; sucrose; galactinol; ds AAV22250 standard; cDNA to mRNA; 2517 (AJIN) AJINOMOTO KK. (first entry) 96JP-0198079 96JP-0107682 97JP-0111124 Location/Qualifiers 56..2410 /product= raffinose_synthase /*tag-ВÞ

transformed

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Best Local S
Matches 2517
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                                                                                                                                             GTTTGCACTTGTTAAAGAGGCGATGAAGATCGTGAGGACCCATCTTGGAACTTTTCGCTT
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62 62	CCTGACTGGGATATGTTCCAATCCACCCACCCTTGTG 	UT UT	Оу
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This is the nucleotide sequence of a mustard cDNA clone coding of a raffinose synthase (see AAY32074), a protein which can bind a D-galactosyl group through an alpha(1-6) bond to the hydroxy group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. The cDNA was isolated from mustard (Brassica Juncea) leaf cDNA by PCR. Probes or primers generated from plant raffinose synthase genes (see AAZ20207-10) may be used to obtain other raffinose synthase genes may be used to control the levels of raffinose produced in plants. Antisense genes can be used to knock out existing gene activity, and sense genes to increase the level of gene activity. The resulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacteria, providing general chealth advantages. The sense and antisense genes may also be used in gene and phenotypic analysis of plants and for the selection of plant clones with the desired characteristics with respect to
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
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               TCCGAAGTATGTTGTATCTTCATGCTGGTGATGATCCGTTTGCACTTGTTAAAGAGGCGGA
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DT 01-02-NOV-2000 EP1048733-A2 Glycine Plant promoter; Soybean raffinose synthase coding sequence SEQ ID 07-MAR-2001 AAC89523; 27-APR-2000; 5 max. standard; 2000EP-0108962 transgenic DNA; entry) 2498 plant; desired

property;

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30-APR-1999; 01-SEP-1999;

99JP-0124527. 99JP-0247211.

(SUMO) SUMITOMO CHEM CO LTD

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residue in a sucrose molecule to form raffinose. The CNA was soluted from sugarbeet cv. haming leaf cDNA by PCR. Probes or PCR primers generated from plant raffinose synthase genes (see AAZ20207-10) may be used to obtain other raffinose synthase genes by labeled detection or amplification (claimed). These genes may be used to control the levels of raffinose produced in plants. Antisense genes can be used to knock out existing gene activity, and sense genes to increase the level of gene activity. The resulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacteria, providing general health advantages. The sense and antisense genes may also be used to in gene and phenotypic analysis of plants and for the selection of plant clones with the desired characteristics with respect to raffinose content.
                                                                                                                                                                                                                                                                                                                                                       This is the nucleotide sequence of a sugarbeet cDNA clone coding for raffinose synthase (see AAY32073), a protein which can bind a D-galactosyl group through an alpha(1-6) bond to the hydroxy group attached to the carbon atom at the 6-position of the D-glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New sense and antisense genes, useful raffinose in food plants -
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Query Match Best Local Similarity Matches 1486; Conserv Conservative 38.8%; Score 976.8; DB 20; pred. No. 3.5e-285; 1; Mismatches 683; Indels Length 2690 30;

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Sequence 2690 BP; 762

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18-DEC-1996;
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                        Claim
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                                                                                                                                                                                      (SUMO ) SUMITOMO CHEM CO LTD
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                          9; Page 27-30; 40pp; Japanese
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Best Local Similarity 65.2
Matches 1536; Conservative
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                                            GAATGAACCAAACCGTCGCCGGCGAGCAAATGCCCTGCCGTCTTTTGAAATTCCAAGAGA 920
                                                                                                    TAATCGACGATGGTTGGCAATCCATCGGACACGATTCGGATCCCATCAC---CAAAGAAG
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 ATTACAAATTCCGTGACTACGTCAATCCCAAGGCCACCGGCCCCGAGCCGGCCAGAAGG
                           gtatgaagcgaacctccgcaggggagcaaatgccatgcaggttggtgaagttggaggaaa
                                                                                   taatcgacgacgggtggcaagccatttgtcacgacgaggaccccataacggaccaagagg
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AAACCTTTGCGCTTTACCTCTATCAAGCCCAAAAAACTTATCCTCTCCAAGCCCTCTCAAG 206	Оу 200	
gagtcccaagacattgaatggagcaatgggaaaagcccaatatgcataaaagggatga	19	
9 gtcccgtaactaggagaaacaagagtgcctctgaattttcacaaaactgtgacatgcttag 1 1 cTaacccaaaacacaTacaaTGCCaCacTGCGACAAAACCCTTATTCTATTGAAGGCGCTTA 2	Db 1889	
GTCGTGAGACACGCCGCAACCAATGCTTTTCACAATACTCAAAACGAGTGACATCCAAAA	18	
tcaacaaatatacaggtgttttgggtct	Db 182	
AATCTCAACAAGTTCACTGGAGTGATTGGTGCATTCAACTGCCAAGGAGGAGGAT	Qy 182	
gagactgtttgtttgaagaccccttg	Db 176	
GTTTGTTTGAAGACCCTTTGCATAATGGAGAAACTATGCTTAAGA	Qy 176	
gcctcgctttgcctgatgggacgattttgcgttgtcaacactatgcact	·	
'GGATCGATCCTTCGAAGTGAGTACTATGCA	Qy 170	
9 999ccatctctg9tg9accagtttacgttagtgattgtgttggaaagcacaacttcaagt 17	Db 164	
AGCCATCTCTGGTGGCCCGATCTATGTTAGTGATTCTGTGGGAAAGCATAAC	Qy 164	
0 agccggattgggacatgttccagtccactcacccttgtgccgaattccatgc-gcctcta 16	Db 159	
ACTGGGATATGTTCCAATCCACCCACCCTTGTGCCGCCTTCCATGCTGCCTC	Qy 158	
.gcactgtgcctacaacagcttgtggatggggaatttta	Db 153	
TCCAAGGATGTCACATGGTTCATTGTGCCAACGACAGCTTGTGGATGGGGAAC	Qy 1521	
0 gcgtaggagatgatttttggtgcactgatccctctggagatccaaatggcacgtattggc 15	Db 147	
TTGGTGATGACTTTTGGTGCACGGACCCCTCTGGTGATCCAAACGGTACGTTTTG	Qy 146	
0 cgagcatggagcattgtaatgacttctttctccttggtaccgaagccatagcccttgggc 14	Db 141	
TATGGAACATTGTAACGACTTCATGTTCCTTGGCACGGAAGCTATCTCTCTTG	Qy 140	
0 cttattacaaagcgctcactgcttcggtgaagaagcatttcaaaaggcaatggggtcattg 14	Db 135	
TTACAAAGCAATGACCAAATCAATAAATAAACATTTTAAAGGAAATGGAGTCA	Оу 134	
	Db 129	
TATCCACCTATTGGAGATGTTGTGTGAAGACTATGGAGGGAG	Qy 128	
0 tgtacgagggctccactcccgtttggaatctgcgggtattgacggtgttaaaggttgacg 12	Db 123	
TACGAAGGACTTCATGCTCATTTGGAAAAAGTTGGGATCGACGGTGTTAAGATTGAC	Qy 122	
0 cggtggataagatcgtcagtaacggagttggactggtgccaccacacctggctcaccttt 12	Db 117	
GTGGATAAGATTGTTCTTCATAAGGTCGGGCTGGTCCCGCCGGAGAAG	Оу 116	
gctaaggttgtcactccgaagctgtccaatggactaaaattgacaatgaaggattta	Db 111	
TGATTCAGCCAGTGCTTTCACCAGGGCTGCAGATGACGATGGAGG	Qy 110	
gtggcacgcgctttgtgggtattggggtggggtcagacccaaggttccgggcatgc	Db 105	
GCATGCTTTGTGGGATATTGGGGTGGCCTTCGCCCGCAGGTGCCTTG	QY 104	
tgttagggacttgaaggaacagtttaggagcgtggagcaggtgtat	Db 99	
GATGAAGGCGTTTATAGATGAACTCAAAGGAGAGTTTAAGACTGTGGAGCATGTTT	0у 98	
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ARESULT ANAHAT A
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                                                                                                                                                   The present invention relates to a mutant protein of raffinose synthas in which at least one aromatic amino acid present at the position of about 1-7 amino acids from the N-terminus is deleted or replaced. The mutant protein can be used for reducing the raffinose oligosaccharide content in a plant body. The present polynucleotide from soybean, was used in the present invention.
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Query Match 38.0 Best Local Similarity 66.0 Matches 1421; Conservative

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                     This sequence encodes the broad bean raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides in the host organism or cell is changed. Raffinose oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
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ω N	ACCTAACGGTTCATCCACAGGGCGTAATAGAAGGCGTGAGGCATCTCGTCGACGGCGGT 7	98
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              GTTCAAGTGCCATGGCCAATTGATTCTTCATCG 2377
                                                                                         gtcaagattggggtgagaggttgcggggagatgagcgtgtttgcgtctgagaaaccggtt
                                                                                                      GTCGAGATTGGTGTCAAAGGGTGTGGTGAGATGCGAGTATTTGCATCGAAAAAACCCAAGG
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                                                                                                                                                    AACATGCTTAACACTAGTGGAGCCATCCAATCTGTGGACTATGACGATGACCTAAGCTCA
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                                           {\tt tgctgcaaaattgatggggttaaggtgaaatttctttatg---aggacaaaatggcaaga}
                                                          GCTTGTCGTATTGATGGGGAGGATGTTGGGTTCAAGTATGATCAGGACCAAATGGTGGTG
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Best Local Similarity
Matches 1421; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                          Claim 6;
                                                                                                                                                                                                                                                                                                                        Sequence 2746
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18-DEC-1996;
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                                                                                                                         TCAGATTC---TGGTCGACCGTATGTTTTCCTTCCTTCCGATCGTTGAGGGACCGTTCCGA
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agtatactaaaagaagcagttaaagtaatccaaactcagttaggaacattcaagactctt
                  GCACTTGTTAAAGAGGCGATGAAGATCGTGAGGACCCATCTTGGAACTTTTCGCTTGTTG
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ilarity 66.6%;
Conservative
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96JP-0338673.
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                        aatcacaatttcaagttgctcaaatctcttgttttgcccgatggttctatcttgcgttgt
                                        gccatatccctcggccgcgtcggagatgatttttggtgctctgatccatctggtgatcca
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ID AADD033
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                                                 22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids and encoded proteins involved in the biosynthesis of raffinose, useful for producing soybean seeds with a reduced raffinose content and therefore improved nutritional quality -
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This sequence encodes the Japanese artichoke raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism

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                                                                       New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
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the content of the raffinose family oligosaccharides in the host
nism or cell is changed. Raffinose oligosaccharides are useful as
additives with beneficial effects on the gastrointestinal flora.
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AAZ10003 standard; cDNA to mRNA; ВP

AAZ10003;

(first entry)

Nucleic encoding þ raffinose synthase protein

Raffinose synthase; plant; sucrose; raffinose;

Stachys sieboldii

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Best Local Similarity
Matches 1223; Conserv
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18-DEC-1996;
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         AGGAATGAACCAAACCGTCGCCGGCGAGCAAATGCCCTGCCGTCTTTTGAAATTCCAAGA
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<u>ggggatgggagaacctccgccggagagcaaatgccctgcaggttgatcaagtttgagga</u>
                                            ggtgttgatcgacgacgggtggcagtccatttgtcacgacaacgacgcgctcaccaccga
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/product= "raffinose synthase"
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                           cgctggtccgagtgacattgagtggaagcaaggaacgagtccgatcgacgtcgacggcgt
                                          AACTAACCCAAAAGACATAGAATGGCACAGTGGAGAAAACCCCTATCTCTATTGAAGGCGT
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       This is the nucleotide sequence of a rapesed cDNA clone coding CC for raffinose synthase (see AAY32075), a protein which can bind a CD -galactosyl group through an alpha(1-6) bond to the hydroxy group cattached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. The cDNA was CI isolated from rapeseed cv. Westar leaf cDNA by PCR. Probes or CPCR primers generated from plant raffinose synthase genes (see CAX20207-10) may be used to obtain other raffinose synthase genes may be used to control the levels of raffinose produced in plants. CPC and sense genes can be used to knock out existing gene activity, CPC and sense genes to increase the level of gene activity. The resulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacteria, providing general CPC health advantages. The sense and antisense genes may also be used in gene and phenotypic analysis of plants and for the selection of CPC plant clones with the desired characteristics with respect to
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10-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local Similarity
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Search completed: December 1, 2001, 02:29:31 Job time: 6058 sec

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ALIGNMENTS

	FEATURES source							COMMENT	JOURNAL		TITLE		AUTHORS	REFERENCE					ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	BF635461
/organism="Medicago truncatula" /db_xref="taxon:3880" /clone="NF080A03DT"	Location/Qualifiers 1. 668	Seq primer: TCACACAGGAAACAGCTATGAC.	_	Fax: 580 221 7380	Tel: 580 221 7391	The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA	Plant Biology Division	Contact: May GD	Unpublished (2000)	Medicago truncatula drought library	Expressed Sequence Tags from the Samuel Roberts Noble Foundation	Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.	Torrez-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,	1 (bases 1 to 668)	Medicago.	Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Medicago truncatula	barrel medic.	EST.	BF635461.1 GI:11899619	BF6,35461	5', mRNA sequence.	NF080A03DT1F1020 Drought Medicago truncatula cDNA clone NF080A03DT	BF635461 668 bp mRNA EST 19-DEC-2000	

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Gossypium hirsutum
Gossypium hirsutum
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Eukaryota; Vagnoliophyta; eudicotyledons; core et
Spermatophyta; Magnoliophyta; eudicotyledons; core et
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium
1 (bases 1 to 646)
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AI727515.1
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/tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entire plantlets harvested in a series of days-post-watering timepoints."
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Cotton fiber Gossypium hirsutum cDNA 5' similar
inose synthase [Cucumis sativus], mrNA sequence.
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Pred. No. 1.2e-83;
0; Mismatches 145
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                                                                        TGCCGCCTTCCATGCTTCCAGCCATCTCTGGTGGCCCGATCTATGTTAGTGATTC
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                TGTTGGCAACCACAACTTTGCTCCTCAAACGCCTCGTNTTACCCGATGGTTCGATCCT
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492; Conser
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Email: burr@bnlux1.bnl.gov
Seq primer: T3 Primer.
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/db_xref="taxon:3635"
/clone_lib="Six-day Cotton fiber"
/tissue_type="immature fiber"
/tay post anthesis"
/dev_stage="Six days post anthesis"
/lab_host="XLI-Blue"
/lab_host="XLI-Blue"
/note="Yector: pBluescript II KS+"
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                                                          CATGCTCATTTGGAAAAAGTTGGGATCGACGGTGTTAAGATTGACGTTATCCACCTATTG 1294
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             ATGACCAAATCAATAAATAAACATTTTAAAGGAAATGGAGTCATTGCAAGTATGGAACAT 1414
                                                                                                                       GTTAATAATGGTGTTGGGTTAGTTCCTCCTCATTTGGTTGATCAAATGTATGAAGGTATT
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CTCTCAACTTCAGTGAAAAAACATTTCAATGGTAATGGTGTCATTGCTAGCATGGAACAT
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BF636478
BF636478.1 GI:1190
EST.
barrel medic.
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Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam woble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
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Eukaryota; Virdiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
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NF089A04DT1F1024 Drought
5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: gdmay@noble.org
Insert Length: 649 Std Error: 0.(
Plate: 089 row: A column: 04
Seq primer: TCACACAGGAAACAGCTATGAC
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Flores,H.R., Inman,J.T., Weller,J.W. and N
Expressed Sequence Tags from the Samuel Rc
Medicago truncatula drought library
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/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture
plantlets harvested in a series of days-post-w
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/organism="Medicago t
/db_xref="taxon:3880"
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An expressed sequence tag database accombryanthemum crystallinum
                                                                                                                                                                                                                                                                                                                                                                                                            Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embry.
Spermatophyta; Magnoliophyta; eudicotyledons;
Caryophyllidae; Caryophyllales; Aizoaceae; Me.
1 (bases 1 to 616)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE131081 616 bp mRNA EST L48-1031T3 Ice plant Lambda Uni-Zap XR expression NaC1 treatment Mesembryanthemum crystallinum cDNA 5', mRNA sequence.
                                                                                                                                                                                               Seq primer: T3
                                                                                                                                                                                                                                                                                                                   Department of Biochemistry University of Nevada
                                                                                                                                                                                                                                                                                                                                               Contact: Cushman JC
                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
                                                                                                                                                                       POLYA-NO.
                                                                                                                                                                                                              Plate: L48-11
                                                                                                                                                                                                                          BACKWARD: T3
                                                                                                                                                                                                                                       FORWARD: T7
                                                                                                                                                                                                                                                   PCR PRimers
                                                                                                                                                                                                                                                                               Fax: 775-784-1650
                                                                                                                                                                                                                                                                                                        MS200,
            177
                                                                                                                                                                                                                                                                                  0, Reno, NV 02.
775-784-1918
                                                                                                                                                                                  quality sequence
                                                                                                                                                                                                                                                                )cushman@unr.edu
      /tissue_type="Leaf, 48 h 0.4M NaCl"
/dev_stage="Six week old"
/note="vector: Lambda Uni-Zap XR, B]
ECORI; Site_2: XhoI"
133 c 144 g 162 t
                                                                            /clone_lib="Ice plant Lambda
, 48 hours NaCl treatment"
                                                                                                   /organism="Mesembryanthemum/db_xref="taxon:3544"
/clone="L48-1031"
                                                                                                                                                        Location/Qualifiers
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                                      Site_1:
                                                                                          library
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Query Match
Best Local Similarity
Matches 458; Conserv

Conservative

14.48;

Score 363.2; DB 1 Pred. No. 9.9e-72; 0; Mismatches 158

10;

Length

616; 0

Gaps

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Gossypium hirsutum
Gossypium hirsutum
Gossypium viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

1 (bases 1 to 515)
1 (bases 1 to 515)
Natralitt W Matz.E.C., Davy,D.F. and Burr,B.
                                                                                                                                                                                                                                                                                                                                                   AI727581 515 bp mRNA EST 11-JUN-1999 BNLGHi8471 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AF073744) raffinose synthase [Cucumis sativus], mRNA sequence
                                Tel: 516-344-3396
Fax: 516-344-3407
Email: burr@bnlux
                                                                Biology Department
Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3396
                                                                                                                                Unpublished (1999)
Contact: Ben Burr
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                                                                                                                                                                                                                                                                                                                    AI727581
AI727581.1
               Seq
               il: burr@bnlux1.bnl.gov
primer: T3 Primer.
                                                                                                                                                                 from developing cotton fiber
Location/Qualifiers
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                                                                                                                                                                                                BF634464 682 bp n
NF061C04DT1F1033 Drought
5', mRNA sequence.
BF634464
                                                                                                Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
           Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gon
Flores,H.R., Inman,J.T., Weller,J.W. and May,
Expressed Sequence Tags from the Samuel Rober
Medicago truncatula drought library
                                                                                                                                                                                    BF634464.1
Unpublished (2000)
                                                                                  Medicago.
                                                                                                                                                        barrel medic.
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                                                                      (bases 1 to 682)
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/cultivar="Acala Maxxa"
/db_xref="taxon:3635"
/clone_lib="Six day Cotton fiber"
/tissue_type="immature fiber"
/dev_stage="Six days post anthesis"
/lab_host="Xit-Blue"
/note="Vector: pBluescript II KS+"
a 96 c 129 g 156 t
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78.8%;
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Pred. No. 2.2e-66;
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             GTCGAGATTGGTGTCAAAGGGTGTGGTGAGATG-CGAGTATTTGCATCGAAAAAACCAAG
                                                                               AACATGCTTAACACTAGTGGAGCCATCCAATCTGTGGACTATGACGATGACCTAAGCTCA 2224
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                                                                                                                                                                                                                                                                                   TCTATTGAAGGCGTTAAAAACCTTTGCGCCTTTACCTCTATCAAGCCAAAAAAACTTATCCTC 2044
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2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
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Insert Length: 682 Std Error: 0.0
Plate: 061 row: C column: 04
Seg primer: TCACACAGGAAACAGCTATGAC.
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Plant Biology Division
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/db_xref="taxon:3880"
/clone="NF061C04DT"
/clone="NF061C04DT"
/clone_type="Plantlets"
/tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entire
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An integrated analysis of the genetics, development, and evolution of the cotton fiber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arboreum cDNA clone GA_Eb0005F08f, mRNA sequence.
BF269676
BF269676.1 GI:11200671
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Fax: 864 656 4293
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100 Jordan Hall, Clemson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Majvales; Malvaceae; Gossypium.
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Seq primer: TAATACGACTCACTATAGGG
High quality sequence stop: 563.
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/db_xref="taxon:29729"
/db_xref="fa__Eb0005708f"
/clone="GA__Eb0005708f"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/clissue_type="Fibers isolated from bolls harvested 7-10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Gossypium arboreum"
/strain="AKA"
                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
143 c 124 g 145 t 3 others
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Asamizu,E., Nakamura,Y., Sato,S.
Generation of 7137 non-redundant
legume, Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
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Lotus japonicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Yasukazu Nakamura
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                                                                                                                                                                                                                                                         124
                                                                                                                                                                                                                                                                                                                                                                                                       1532-3, Kisarazu, Chiba 292-0812, Japan
l: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                      /organism="Lotus japonicus"
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a 117 c 119 g 129 t
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                                                                                                                                                                                 11.7%;
75.5%;
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                                                                                                                                                                   Score 295.6; DB 10;
Pred. No. 1.9e-56;
0; Mismatches 119;
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KF090H02DT1F1027 Drought Medicago

5', mRNA sequence.

BF636592
                                                                                                                                                                                              Email: gdmay@noble.org
Insert Length: 513 Std Error: 0.0
Plate: 090 row: H column: 02
Seq primer: TCACACAGGAAACAGCTATGAC
                                                                                                                                                                                                                                                             2510 Sam Noble Parkway, Ardmore,
Tel: 580 221 7391
Fax: 580 221 7380
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                                               /tissue_type="plantlets"
/dev_stage="pooled timepoints"
/note="vector: Lambda Zap; Conta
plantlets harvested in a series
                                                                                                                       /organism="Medicago truncatula"
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                    timepoints.
72 c
                                                                                                           /clone_lib="Drought"
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Query Match

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                                                                                                      E 1 (bases 1 to 818)

Singh, J.A., Wakul, K., Couroux, P., De Moors, A., Harris, L.J., Hat J.I., Ouellet, T., Robert, L.S., Sprott, D. and Tinker, N.A. Expressed Sequence Tags from Cold-Stressed Maize Seedlings Unpublished (2001)
Contact: Singh, J.A.
Eastern Cereal and Ollseed Research Centre Agriculture and Agri-food Canada 960 Cariing Avenue, Bldg. 20, Ottawa, Ontario, KlA 0C6, Canada Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@em.agr.ca.
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Zm04_D5d11_R Zm04_D5CDRC_CONC_COLd_stressed_maize_seedlings
cDNA clone Zm04_05d11, mRNA sequence.
BG321136
BG321136.1 GI:13150814
                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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                                                                                         singhja@em.agr.ca.
Location/Qualifiers
/db_xref="taxon:4577"
/clone="zm04_05d11"
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/tissue_type="Leaf, crown"
                                                    /organism="Zea mays"
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                                                                                    TCACTGTTTCACCAGTGACC---AAACTCATCCAAACTTCTCTACACTTTGCCCCCAATTG
                                                                                                                                                                                                                                                                                           CGAGTGACATCCAAAACTAACCCAAAAAGACATAGAATGGCACAGTGGAGAA-----AACC
                                                                                                                                                                                                                                                                                                                                                            CAAGGAGGAGGATGGTGTGGTGAGACACGCCGCAACCAATGCTTTTCACAATACTCAAAA
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GACTCGCCAACATGCKCAACACCGCCGGCGCCC
                                 GGCTGGTGAACATGCTTAACACTAGTGGAGCC 2186
                                                                     TCGTCGTCGCCCCTTKCGCKTYAWCTCGCACGAGCGGGCCATYWWGTTCGCKCCCATCG
                                                                                                                                    AGCYGCTGCGCCCGACGAGGGCGTCGACCTCACGCTGCAGCKCTTCACCTACGAKCTCT
                                                                                                                                                                  TCCTCTCCAAGCCCTCTCAAGATCTTGACATAGCTCTTGACCCATTCGAATTCGAGCTCA
                                                                                                                                                                                                        GGCGTCACTTTTWGGGCGTCTCCCAGTTCGCCGTGTACYCCGTCGAGGCCAGGACGCTGC
                                                                                                                                                                                                                                      CTATCTCTATTGAAGGCGTTAAAACCTTTGCGCTTTACCTCTATCAAGCCAAAAAACTTA
                                                                                                                                                                                                                                                                         CCCCTTGCCGCGCGCGCCTCGCCGTCCGACGTCGAATGGAAGARCGGCAAARCGGGACCA
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Similarity 58.3%;
73; Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Vector: Bluescript SK-/XhoI-EcoRI; Site_1: Eco Site_2: Xho I; Lower temperature 50 C / hour from 22 t 120C; bring to 50 in 1 hour from 120C. Leave at 50C 2, photoperiod 16 hours. Light intensity was 125 uE-1. Library, prepared by in vivo mass excision from amplifit library."

230 g 129 t 47 others
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Pred. No. 1.4e-51;
32; Mismatches 298
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Best Local
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                                                                                    1542 ATTGTGCCAACGACAGCTTGTGGATGGGGAACTTCATCCACCCTGACTGGGATATGTTCC
                                                             N
AATCCACCCACCCTTGTGCCGCCTTCCATGCTGCCTCTCGAGCCATCTCTGGTGGCCCGA 1661
                                                          BF425566 525 bp mRNA EST 31-JUL-2001 su44c11.y1 Gm-c1068 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1068-2061 5' similar to TR:Q9ZT62 Q9ZT62 RAFFINOSE SYNTHASE ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, 1
Tel: 314 286 1800
Fax: 314 286 1810
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BF425566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or info@genomesystems.com web site: www.genomesystems.com
Insert Length: 1160 Std Error: 0.00
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Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from drought stressed leaf tissue of the cultivar Williams 82. The month old greenhouse grown plants were deprived of water for 3 days prior to harvesting the stressed leaf tissue. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a xhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by xhoI digestion. The cDNA fragments were directionally cloned into the EcoRI. YhoI restriction site of the pBluescript vector. The
                                                                                                                                                                                                                                                                                                                                           ligated cDNA fragments were transformed into DH10B cells (GibcoBRL). This library was constructed in t laboratory of Dr. Randy Shoemaker."

132 c 118 g 139 t 4 others
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/clone_lib="Gm-c1068"
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701496022 A.
CDNA clone 70
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                                                                                                                                                                                                                                                                                              Genome Systems, Inc., a wholly Pharmaceuticals, Inc.
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                                                                                                                                                                                                        service@genomesystems.com
Location/Qualifiers
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                                                                 Arabidopsis
                                                             /clone_lib="A. thaliana, Ohio State clone set"
/note="cDNA library was made from selected clones
Arabidopsis thaliana Ohio State clone set."
115 c 128 g 155 t
                                                                                                                                                   /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
                                                                                                                                      /clone="701496022"
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Query Match

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                                                                                                                                                                               Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzale Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts N Medicago truncatula drought library Unpublished (2000)
Contact: May GD
                                                                                                                                                                                                                                                                                                                                                                                                             BF633327 435 bp mrNA
NF054D03DT1F1028 Drought Medicago
5', mRNA sequence.
BF633327
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                       2510 Sam Noble Parkway, Ardmore,
Tel: 580 221 7391
Fax: 580 221 7380
                                           Email: gdmay@noble.org
Insert Length: 435 Std Error: 0.0
Plate: 054 row: D column: 03
Seq primer: TCACACAGGAAACAGCTATGAC
                                                                                                                                                                 Plant Biology Division
                                                                                                                                                                                                                                                                                          Medicago.
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                                                                                                                                     Samuel Roberts Noble Foundation
Samuel Roberts Noble Foundation
OK
1. .435
/organism="Medicago truncatula"
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AUTHORS
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                                                        Euphorbia ésula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Malpighiales; Euphorbiaceae; Euphorbia.
1 (bases 1 to 486)
Anderson, J.V. and Horvath, D.P.
Identification of mRNAs expressed in underground adventitious buds of Euphorbia esula (leafy spurge)
Unpublished (2000)
Contact: Anderson JV
                                                                                                                                                                                                                                                                                    AW944715 486 bp
00168 leafy spurge Lambd
Library Euphorbia esula
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                             USDA/ARS, Biosciences
                                               Plants Science Research
                                                                                                                                                                                                            leafy spurge.
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   Albrecht Blvd.,
701 239 1263
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/clone_lib="Drought"
/tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plantlets harvested in a series of days-post-watering
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Pred. No. 2.1e-49;
                               Research Lab
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Best Local Sim
Matches 345;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTTGGAAAAAGTTGGGATCGACGGTGTTAAGATTGACGTTATCCACCTATTGGAGATGT 1301
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1 (bases 1 to 591)
1 (bases 1 to 591)
2 Noemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, v., A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Na, Bolla, B., Marra, M., Steptoe, M., Theising, B., Allen, M., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., V., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
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BG043590.1
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Email:
Seq pr:
                                                                                                                                                                                                                                                                                 BG043590 591 bp mrNA EST 31-JUL-2001 Su40f05.y1 Gm-c1068 Glycine max CDNA clone GENOME SYSTEMS CLONE II Gm-c1068-1809 5' similar to TR:09SBZ0 Q9SBZ0 GALACTINOL-RAFFINOSE GALACTOSYLTRANSFERASE;, mRNA sequence.
                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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/clone="24F"
/clone_lib="leafy spurge Lambda HybriZAP 2.1 two-hybrid vector cDNA Library"
/tissue_type="underground adventitious buds"
/dev_stage="3-day induced (decapitated)"

92 c 131 g 137 t
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Pred. No. 2.6e-49;
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                                                                                                                                                                                                                                                                        AAGACTATGGAGGGAGAGTGGATTTGGCAAAGGCATATTACAAAGCAATGACCAAATCAA 1367
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ACCCCTCTGGTGATCCAAACGGTACGTTTTGGCTCCAAGGATGTCACATGGTTCATTGTG
                                                                                                                                                                                                       TAAATAAACATTTTAAAGGAAATGGAGTCATTGCAAGTATGGAACATTGTAACGACTTCA 1427
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                                                                                                                                                                                                                                                                                                                                                                         AAAAAGTTGGGATCGACGGTGTTAAGATTGACGTTATCCACCTATTGGAGATGTTGTGTG 1307
                                                                              TCTTCCTTGGAACCAAGCAAATTCCCCATGGGAAGAGTTGGGGATGACTTTTGGTTCCAAG
                                                                                                                                                                  TTGTCAAGAATTTTAATGGAAGTGGAATCATCGCTAGCATGCAGCAGCGCAACGACTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available through: Genome Systems, Inc. 4633 parkway Circle St. Louis, Missouri 63134 For further infor call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 427-3324 or contact: clones@genomesystems.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
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Contact: Shoemaker R/Public
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from drought stressed leaf tissue of the cultivar Williams 82. The month old greenhouse grown plants were deprived of water for 3 days prior to harvesting the stressed leaf tissue. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."
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/clone="orxnon:"
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/clone_lib="Gm-c1068"
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US-09-477-046B-5
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14, Appl
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19, Appl
19, Appl
19, Appl
19, Appl
11, Query Match 100.0%; Score 2517; Best Local Similarity 100.0%; Pred. No. 0; Matches 2517; Conservative 0; Mismatches
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US-	000000000000000
RESULT US-08-84 Sequen Patent GENERA NUM NUM COR N S CC C	8600 12 8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
1 1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	33.6 1.3 4377 4 US-09-479-409-28 Sequence 28, 33.4 1.3 1505 1 US-07-915-246-1 Sequence 1, 33.4 1.3 1505 1 US-07-915-246-1 Sequence 1, 33.4 1.3 34303 2 US-08-735-609-4 Sequence 28, 33.1.3 34303 2 US-08-735-609-4 Sequence 4, 33.1.3 34303 3 US-09-244-752-4 Sequence 4, 33.1.3 34303 3 US-09-245-497-4 Sequence 4, 33.1.3 34303 3 US-09-245-497-4 Sequence 4, 33.1.3 34303 3 US-09-245-497-4 Sequence 6, 33.1.3 35408 4 US-08-973-334-3 Sequence 3, 35408 4 US-08-973-334-3 Sequence 3, 35408 4 US-08-735-609-1 Sequence 3, 35408 4 US-08-735-609-1 Sequence 1, 33.1.3 35935 3 US-08-379-452-43 Sequence 1, 33.1.3 35935 3 US-09-315-372-1 Sequence 1, 33.1.3 35935 3 US-09-315-372-1 Sequence 1, 33.1.3 35935 3 US-09-245-497-1 Sequence 1, 33.1.3 35935 3 US-09-245-497-1 Sequence 1, 34.11GNMENTS
	Appl Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli

DB 0 4

Length 2517;

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960	TCTTTTGAAATTCCAAGAGAATTACAAATTCCGTGACTACGTCAATCCCAAGGCCACCGG	901 901
900	GGATCCCATCACCAAAGAAGGAATGAACCAAACCGTCGCCGGCGAGCAAATGCCCTGCCGGGATCCCATCACCAAAGAAGAAGAACCAAACCGTCGCCGGCGAGCAAATGCCCTGCCGGGAATCAACCAAAACAAAC	841 841
840 840	CGGTTGTCCTCCCGGTTTAGTCCTAATCGACGATGGTTGGCAATCCATCGGACACGATTC	781 781
780 780	GTTTTACCTAACGGTTCATCCACAGGGCGTAATAGAAGGCGTGAGGCATCTCGTCGACGG 	721 721
720 720	GTTGGAGGAGAAGACTCCACCAGGTATCGTGGACAAATTCGGTTGGTGCACGTGGGACGC 	661 661
660 660	GTTTGCACTTGTTAAAGAGGCGATGAAGATCGTGAGGACCCATCTTGGAACTTTTCGCTT 	601
600	GTCGAAAGTTGTTGATGCATCGTTCCGAAGTATGTTGTATCTTCATGCTGGTGATGATCC	541 541
540 540	CCGAACCTCGATTCAGCCTGGGGATGATGACTTTGTCGATGTTTGTGTCGAGAGTGGTTC	481 481
480 480	TGAGAAGTCAGATTCTGGTCGACCGTATGTTTCCTTCTTCCGATCGTTGAGGGACCGTT	
420 420	GGAGACTCAGATTGTGATCCT	361 361
360 360	GATTGGGAAGCTGAAGGATATTCGGTTTATGAGTATTTTCAGGTTTAAGGTTTGGTGGAC 	301 301
30C	TTCGGTTGGTTGCTTTGTTGGATTCGACGCGTCGGAACCTGATAGCCGACATGTTGTTTC	241 241
240 240	TGTTCCTGAGAACATTGTTGCTTCTCCTCTCTCCGTACACTTCGATAGACAAGTCCCCGGT	181 181
180 180	GTCACCGTTTGCAATCGACGGATCGGATTTCACTGTGAACGGTCATTCGTTTCTGTCCGA 	121 121
120 120	TCCTAGTTTTAAAAATGGTGGCTCCAACGTAGTTTCATTTGATGGCTTAAATGACATGTC	61
60	AAAAAACAACCCTTCTTTAGTTTTTTGGGTTTGTTTCTTCTTTTTTTT	1 1

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GGTGAACATGCTTAACACTAGTGGAGCCATCCAATCTGTGGACTATGACGATGACCTAAG 222	ACTETTTCACCAGTGACCAAACTCATCCAAACTTCTCTACACTTTGCCCCAATT6GGCT 21	21	AG:	CCTCTCCAAGCCCTCTCAAGATCTTGACATAGCTCTTGACCCCATTCGAAGTTCGAGCTCAT 2100	TATCTCTATTGAAGGCGTTAAAACCTTTGCGCTTTACCTCTATCAAGCCAAAAAAACTTAT 2040	AAAACCC 1	GAGTGACATCCAAAACTAACCCAAAAG		TGCCAAGGAGGAGGATGGTGTCGTGAGAC	AGAAACTATGCTTAAGATTTGGAATCTCAACAAGTTCACTGGAGTGATTGGTGCATTCAA 1860	TTTGAAGACCCTTTGCATAATGG 18	AAGTGAGTACTATGCACTCCCGACTCGCGATTGTTTGTTT	GGGAAAGCATAACTTTGATCTTCTGAAAAAACTAGTGCTTCCTGATGGATCGATC	TIC		CGCCTTCCATGCTGCCTCTCGAGCCATCTCTGGTGGCCCGATCTATGTTAGTGATTCTGT 168		CAACGACAGCII IS	TCCAAACGGTACGTTTTGGCTCCAAGGATGTCACATGGTTCATTGTGCCCAACGACAGCTT 156	rcreerea 15	GGAAGCTATCTCTCTGGTCGTGTTGGTGATGACTTTTGGTGCACGGACCCCTCTGGTGA 1500	TAAAGGAAATGGAGTCATTGCAAGTATGGAACATTGTAACGACTTCATGTTCCTTGGCAC 1440	TAAAGGAAATGGAGTCATTGCAAGTATGGAACATTGTAACGACTTCATGTTCCTTGGCAC 144		GAGAGTGGATTTGGCAAAGGCATATTACAAAGCAATGACCAAATCAATAAAATAAACATTT 1380	CGACGGTGTTAAGATTGACGTTATCCACCTATTGGAGATGTTGTGTGTAAGACTATGGAGG 1320	CGACGGTGTTAAGATTGACGTTATCCACCTATTGGAGATGTTGTGTGAAGACTATGGAGG 1320	GCCGGAGAAGGCTGAGGAGATGTACGAAGGACTTCATGCTCATTTGGAAAAAGTTGGGAT 126	GCCGGAGAAGGCTGAGGAGTGTACGAAGGACTTCATGCTCATTTGGAAAAAAGTTGGGAT 126		GATGACGATGGAGGATTTGGCGGTGGATAAGATTGTTCTTCATAAGGTCGGGCTGGTCCC 1200	GCAGGTGCCTGGCTTGCCTGAGGCACGTGTGATTCAGCCAGTGCTTTCACCAGGGCTGCA 114

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TELEFAX: (700,700)
TELEX: 899149
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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US-08-232-463-14/c
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US-08-232-463-14
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                                                                                                                                                                                                     FILING DATE:

APPLICATION NUMBER: EP 91 114 300.6

FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: BENT Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 30472/114 IMMU

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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              IMMEDIATE SOURCE:
CLONE: pTZgpt-F1s
                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1
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TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
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                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTGTTTTAATTTTATGTAAGCTCAATGATTGTTGTTGTTGTCGCTGTTGTTGCT 2460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTGGTTCAAGTGCCATGGCCAATTGATTCTTCATCGGGTGGCATTTTCGGTTATCGAGTA 2400
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1800 Diagonal Road,
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
ZIP: 22313-0295
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy di
                                                                                                                                                 REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 890140
                                                              TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                   FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION UMBER: 29,768
REFERENCE/DOOWER 29,768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKMER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1056 CCCTCGACCTGCAGCCA 1040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 1.9%; Score 47.4; DB 1;
Local Similarity 4.7%; Pred. No. 0.0005;
hes 15; Conservative 178; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                   LENGTH:
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ucleic acid
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; STRANDEDNESS: sinc
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14
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; NAME/KEY: intron
; LOCATION: (187)..(297)
US-09-118-319-1
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Patent No. 6114158
GENERAL INFORMATION:
APPLICANT: L1, Xin-Liang
APPLICANT: L-Jungdahl, Lars G.
APPLICANT: L-Jungdahl, Lars G.
TITLE OF INVENTION: Orpinomyces Cellulase Celf Protein and Coding Sequences
FILE REFERENCE: 33-98sequence listing
CURRENT APPLICATION NUMBER: US/09/118,319
CURRENT FILING DATE: 1998-07-17
NUMBER OF SEQ ID NOS: 9
COCRETE TO COMMERCE OF COMM
sequence 19, Application US/09457046B
Patent No. 6287835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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TYPE: DNA
ORGANISM: Orpinomyces sp. PC-2
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                                                                                                                                                                                                                                                                                                                        TTGTTATCATTGTTATTATTGTTAGAAGCA 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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163; Mismatches 105;
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APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Pacl
FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT ETLING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SOCTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 911
TYPE: DNA
ORGANISM: Taxus cuspidata
US-09-457-046B-19
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                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: 911
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APPLICANT: Croteau, Rodney et al.
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                                                                                                                                                                                                               Matches 116;
                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway FILE REFERENCE: 53679
                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Taxus cuspidata
                                                                                                                                                      372 TTGGTCGAAATGGTGGGGATCTTGAATCGGAGACTCAGATTGTGATCCTTGAGAAGTCAG
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                       492
                                                                                                                                 461 ttgttataaatgttgacaccatagaatatatgaaacaatgtgttatggaggaatgtaatg
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TTCAGCCTGGGGATGACTTTGTCGATGTTTGTGTGTGGAGAGTTGGTTCGTCGAAAGTTG 551
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                                                      atttttgttcgtcctttgaagtagtggcagcattggtttggatagcaaggacaaaggctc 580
                                                                                            ATTCTGGTCGACCGTATGTTTTCCTTCCTTCCGATCGTTGAGGGACCGTTCCGAACCTCGA 491
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milarity 47.2%;
Conservative
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                                                                                                                                                                                                                                   Score 38;
Pred. No.
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US-08-928-361B-2/c
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RESULT 8
US-08-928-361B-1/c
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MOLECULE TYPE:
US-08-928-3618-2
                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                   2397 AGTACTTGTTTTAATTTTATTGTAAGCTCAATGATTGTTGTTGTTGTTGTTGTTGTTGT 2456
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 5511 base pairs
TYPE: nucleic acid
                                                                                   2457 TGCTATCAATGTATTTCT 2474
                                                                                                                                  NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             612 TTAAAG 617
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94306-1840
                                                                                                                                                                                                  Local Similarity
wes 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Palo Alto
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                                                                  TGGTTTCTTGGTAGTTGT 1117
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                                                                                                                                                                                                 Score 36.4; DE Pred. No. 1.1; 0; Mismatches
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                                                                                                                                                                                                                                   RESULT
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                                                                                                                                                              Sequence 3, Application US/09010928B Patent No. 5994099 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                     2397
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COMPUTER READABLE FORM:
                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                      2802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 7334 base pair
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                   2457 TGCTATCAATGTATTTCT 2474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Verny, Hana REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                 ADDRESSEE: BIRCH, STEWART, STREET: 8110 GATEHOUSE RD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                    TGGTTTCTTGGTAGTTGT 2785
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FALLS CHURCH
VIRGINIA
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APPLICANT: Lewis, Randolph V
APPLICANT: Hayashi, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
TITLE OF INVENTION: CODING THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNAY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UNMBER: US/08/928,361B FILING DATE: 12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTACTTGTTTTAATTTTATGTAAGCTCAATGATTGTTGTTGTTGTCGCTGTTGT 2456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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STEWART, KOLASCH & BIRCH
HOUSE RD. SUITE 500E
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COUNTRY:

UNITED STATES OF AMERICA

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                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09383630A Patent No. 6265632 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1140 AGATGACGATGGAGGATTTGGCGGTGGATAAGATTGTTCTTCATAAGGTCGGGCTGGTCC 1199
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ATTORNEY/AGENT INFORMATION:
NAME: MUIPHy Jr., Gerald M
REGISTRATION NUMBER: 28977
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OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                             COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Siimnote-890TX
                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina STREET: 2001 Jefferson Davis Highway, Suite 207
                                                                                                                                                                                                                                                               APPLICANT: Avner Yayon et al.
TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH
FACTOR RECEPTOR ASSOCIATED
                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGCGGAGCTGGAGGACCTGGTGGAGCATACGGACCTGGTGGATCATATGGACCTGGTGG 1037
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                                                                                                     CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
OPERATING SYSTEM: MS DOS version 6.2,
Windows version 3.1
                                                                                           ZIP:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.48; 52.78;
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taken from 3' region. Stop codon begins at position
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Pred. No. 0.95;
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GENERAL INFORMATION:
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Best Local S
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INFORMATION FOR SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          797 TTAGTCCTAATCGACGATGGTTGGCAATCCATCGGACACGATTCGGATCCCATCACCAAA 856
              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,630A
FILING DATE: 26-Aug-1999
CLASSIFICATION: <Unknown>
                                                                                                                              ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

COMPUTER: Twinhead* Slimnote-890TX

OPERATING SYSTEM: MS DOS version 5.2,

Windows version 3.11

SOFTWARE: Word for Windows version 2.0 converted
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APPLICATION NUMBER: US/09/383,630A
FILING DATE: 26-Aug-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH FACTOR RECEPTOR ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Friedmam, Mark M
PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Avner Yayon et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAACCCTGGACTACTGCGCCCGGGGGATCTGCAGCCCGGGGGATCCACTAAGATCCCCT 4858
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                                                                                                                                                                                                                                                                                                                    CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                 COUNTRY: United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 1402/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Word for Windows version 2.0 to an ASCI file
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: <Unknown>
APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.4%;
                                                                                                           to an ASCI file
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.9;
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APPLICATION NUMBER: <Unknown> FILING DATE: <Unknown>

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08209747 Patent No. 5733771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
TELEFAX: 703-205-8050
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4977 TTTGTCCTCAACCGCGAGCTGTGGAAAAAAAGGGACAGGATAAGTATGACATCATCAAG 4918
                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4857 AAGGGTTACTGTCTCCCACACTAAGCACCAGCAGGGGCTTGCCTCACCAAG 4806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4917 GAAACCCTGGACTACTGCGCCCGGGGGATCTGCAGCCCGGGGGATCCACTAAGATCCCCT 4858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                 CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Colgin, Mark
TITLE OF INVENTION: cDNAs Encoding Minor Ampullate Spider
TITLE OF INVENTION: Silk Proteins
                                                           REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 14
REFERENCE/DOCKET NUMBER: 11
REFERENCE/DOCKET NUMBER: 11
REFERENCE/DOCKET NUMBER: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     857 GAAGGAATGAACCAAACCGTCGCCGGCGAGCAAATGCCCTGCCGTCTTTTGAAATTCCAA 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         797 TTAGTCCTAATCGACGATGGTTGGCAATCCATCGGACACGATTCGGATCCCATCACCAAA 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 917 GAGAATTACAAATTCCGTGACTACGTCAATCCCAAGGCCACCGGCCCCCGAG 968
                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Birch, Sto
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
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Local Similarity 50.6%;
hes 87; Conservative
                                                                                                                         NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,97
                                                                                                                                                                                                         APPLICATION NUMBER: US/01 FILING DATE: 14-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: 972-3-5625553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Friedmam, Mark M.
REGISTRATION NUMBER: 33,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                                                                                                   22040-3487
                                                                                                                                                                                                                                                                                                                                                                                                                         Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 972-3-5625554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lewis, Randolph V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stewart, Kolasch & Birch
                                                                                                                                                                                                                                 US/08/209,747
                                                                                                        1447-104P
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                                                                                                                                                                                                                                                                           Version #1.25
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OTHER INFORMATION: /product= "N. clavipes minor; OTHER:INFORMATION: ampullate silk protein"
US-08-209-747-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
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             TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lewis, Ra
APPLICANT: Colgin, M
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                             NAME: MUTPHY JT., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 14-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                       APPLICATION NUMBER: US 08/209,747 FILING DATE: 14-MAR-1994 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1144 GACGATGGAGGATTTGGCGGTGGATAAGATTGTTCTTCATAAGGTCGGGCTGGTCCCGCC 1203
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ORGANISM: Nep
                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/458,298
FILING DATE: 02-UW-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Birch, St. STREET: P.O. Box 747 CITY: Falls Church
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nes 77; Conserv
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   ENGTH:
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2793 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lewis, Randolph V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNAs Encoding Minor Ampullate Spider Silk Proteins
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Pred. No. 1.3;
                                                                                                                     1447-104P
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US-08-425-069-1
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Best Local Similarity
Matches 77; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1144 GACGATGGAGGATTTGGCGGTGGATAAGATTGTTCTTCATAAGGTCGGGCTGGTCCCGCC 1203
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1679 GGTGCCGGAGCAGGAGCTGGTGCGGCTGCTGCTGGTGCAGGAGCAGGAGGTGCTGGT 1738
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                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSE: Birch, Stewart, Kolasch &
STREET: 301 No. 5728810th Washington
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1204 GGAGAAGGCTGAGGAGATGTACGAAG 1229
                                                                                                                                                                                                                                  FILING DATE: 19-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2338 base pairs
                                                                                                                                                     REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-106P
TELECOMMUNICATION INFORMATION:
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LOCATION: 183..2675
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STRANDEDNESS:
                                                                                                              TELEFAX: (703) 205-8050
                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/425,069 FILING DATE: 19-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                    NAME: Murphy Jr., Gerald M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAGGTGCAGGAGCAGGAGCTGGAGG
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Y: U.S.A.
                    nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.48; 52.78;
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Pred. No. 1.3;
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Washington Street
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                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Lewis, I
APPLICANT: Xu, Minc
APPLICANT: Hinman,
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08317844B Patent No. 5989894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: /POTHER INFORMATION: dr. PUBLICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1281 AGGTGGATTAGGTGGACAAGGGGCAGGTGCAGCAGCCGCTGCAGCAGCTGGAGGTGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1083 AGGTGCCTGGCCTGAGGCACGTGTGATTCAGCCAGTGCTTTCACCAGGGCTGCAGA 1142
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch &
STREET: 301 No. 5989894th Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1461 ACGAGGTGGACA 1472
                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1263 ACGGTGTTAAGA 1274
ATTORNEY/AGENT INFORMATION:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAGES: 7120-7124
DATE: Sept.-1990
RELEYANT RESIDUES IN SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Nephilia clavipes
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                                                                                                                                                                                  CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VOLUME:
                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE: Structure of a protein superfiber:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS: Xu, Ming
AUTHORS: Lewis, R
               FILING DATE: 0. CLASSIFICATION:
                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCAGCAGCTGGAGGTGCCGGACAAGGAGGATATGGAGGTCTTGGAAGCCAAGGTGCTGG
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                                                                                                                                                                                                                                                                                                                                                                           Xu, Ming
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dragline silk protein"
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Pred. No. 1.5;
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Washington Street
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                                                                                      Version #1.25
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NAME: Murphy Jr., Gerald M REGISTRATION NUMBER: 28,977

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Search completed: December 1, 2001, 02:25:17 Job time: 6027 sec
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Best Local Similarity 49.0%; Pred. No. 1.5;
Matches 94; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (703) 241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2338 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                              1341 ACAAGGAGGATATGGAGGCCTTGGAAACCAAGGTGCTGGACGAGGTGGACAAGGTGCAGC 1400
                                                                                                                                                                                                                                                                                                                       1461 ACGAGGTGGACA 1472
                                                                                                                  1263 ACGGTGTTAAGA 1274
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                                                                                                                                                                                           1203 CGGAGAAGGCTGAGGAGATGTACGAAGGACTTCATGCTCATTTGGAAAAAGTTGGGATCG 1262
                                                                                                                                                                                                                                                                        1143 TGACGATGGAGGATTTGGCGGTGGATAAGATTGTTCTTCATAAGGTCGGGCTGGTCCCGC 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: CDS
LOCATION: 1..2154
OTHER INFORMATION: /product= "nephila clavipes
OTHER INFORMATION: dragline silk protein"
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 1447-105P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YOUNNAL: Proc. Natl. Acad. Sci.
VOLUME: 87
PAGES: 7120-7124
DATE: Sept.-1990
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS: Xu, Ming
AUTHORS: Lewis, Randolph V.
TITLE: Structure of a protein superfiber:
TITLE: drafline silk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (703) 241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Nephilia clavipes
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Minimum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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/SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*

/SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*

/SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*

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Gapop 10.0 , Gapext 0.5
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AAW57887
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AAW57866
AAX30142
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Sugarbeet raffinos
Soybean raffinose
Amino acid sequenc
Soybean raffinose
Soybean protein: S
Broad bean raffino
Amino acid sequenc
                                                                                                                                                                                                                                            Description
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Cucumber raffinose
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Plasmodium falcipa	AAB18224	21	679		102	44
Arabidopsis thalia	AAG64151	22	933		104	43
Cucumber raffinose	AAY17423	20	19		105	42
Cucumber raffinose	AAW53568	19	19		105	41
Human bone marrow	AAM00916	22	1637	•	106	40
Human bone marrow	AAM00803	22	1080	•	106	39
Rat CARD-6 protein	AAB20088	22	905		106.5	38
3	AAW09043	18	1174	2.5	107	37
B.t. toxin 81A2.	AAR89494	17	1174	٠	107	36
B.thuringlensis to	AAR08257	11	1174	•	107	3 5
Lettuce resistance	AAW64169	19	488	•	107	34
Lettuce resistance	AAW64182	19	487	•	107	ω
Photorhabdus lumin	AAY33727	20	1584	•	107.5	32
Grapevine leafroll	AAW21636	18	1390	•	109	31
Novel toxin expres	AAR25825	13	1174		111	30
Arabidopsis thalia	AAG28630	21	120	٠	177.5	29
Cucumber raffinose	AAY17422	20	30		181	28
Cucumber raffinose	AAW53567	19	30	•	181	27
	AAG28629	21	193	•	263.5	26
Arabidopsis thalia	AAG28628	21	229	•	389.5	25
Amino acid sequenc	AAY30145	20	271		788	24
Corn raffinose syn	AAW57889	19	271		788	23
Soybean raffinose	AAY32072	20	265		873	22
Corn raffinose syn	AAY70974	21	508	22.2	940	21
Rice raffinose syn	AAY70976	21	770	•	1384	20
õ	AAY17418	20	750	•	1394	19
Wheat raffinose sy	AAY70981	21	841	•	1398.5	18
Corn raffinose syn	AAY70975	21	756	33.9	4	17
	AAY70977	21	763	•	1470	16
Wheat raffinose sy	AAY70980	21	751	•	1490	15
Rapeseed raffinose	AAY32075	20	572	٠	2364	14
-	AAY30144	20	587	59.9	2529	13
Japanese artichoke	AAW57888	19	587	59.9	2529	12

ALIGNMENTS

RESULT AAW53570

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AAW53570;

AAW53570 standard; Protein; 784

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Cucumber raffinose synthase.
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The present sequence is cucumber raffinose synthase, which
                                                                                                                                                                       Claim 3; Pages 17-20; 26pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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Matches 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cucumber raffinose
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30-APR-1998;
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This sequence represents mustard raffinose synthase, a protein that can bind a D-galactosyl group through an alpha(1-6) bond to the hydroxy group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. cDNA (see AAZ20209) encoding the enzyme was isolated from mustard
                                                                                                                                 Claim
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                                                                                                                                                                                            and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthase; mustard;
                                                                                                                                                                         food plants
                                                                                                                                                                                                                                                                                                  Oeda K;
                                                                                                                                                                                                                                                                                                                                                                                     98JP-0120550.
98JP-0120551.
98JP-0345590.
98JP-0351246.
                                                                                                                             29-31; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99EP-0107430
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Best Local Similarity
Matches 555; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Brassica juncea) leaf cDNA by PCR. Probes or primers generated from plant raffinose synthase genes (see AAZ20207-10) may be used to obtain other raffinose synthase genes by labeled detection or amplification (claimed). These genes may be used to control the levels of raffinose produced in plants. Antisense genes can be used to knock out existing gene activity, and sense genes to increase the level of gene activity. The resulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacteria, providing general health advantages.
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                                                                                                                                                                                                                                                                                                                                                                                                                                map----psviksdaavngidlsgkplfrlegsdllanghvvltdvpvnvtvtaspyl 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAPSFKNGGSNVVSFD----GLNDMSSP-FAIDGSDFTVNGHSFLSDVPENIVASPSPY-
   SSSGGISVIEYLF
                                                                                                                                                                                                                                                          frdyvspk----dknevgmkafvrdlkeefstvdyiyvwhalcgywgglrpgaptlppst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             777 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.9%; Score 2996.5; DB 20; 70.0%; Pred. No. 1.2e-274; tive 99; Mismatches 114; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents sugarbeet raffinose synthase, a protein that can bind a D-galactosyl group through an alpha(1-6) bond to the hydroxy group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. CDNA (see AAZ20208) encoding the enzyme was isolated from sugarbeet cv. haming leaf cDNA by PCR. Probes or primers generated from plant raffinose synthase genes (see AAZ20207-10) may be used to obtain to ther raffinose synthase genes by labeled detection or amplification (claimed). These genes may be used to control the levels of raffinose produced in plants. Antisense genes can be used to knock out existing gene activity, and sense genes to increase the level of gene activity. The resulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacteria, c providing general health advantages.
                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-APR-1998;
30-APR-1998;
04-DEC-1998;
10-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Watanabe E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SUMO ) SUMITOMO CHEM CO LTD
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SIDKSPVSVGCEVGEDASEPDSRHVVSIGKLKDIRFMSIFREKVWWTTHWVGRNGGDLES
                                                                                                                                    MAPSFKNGGS----NVVSFDGLNDMSSP-FAIDGSDFTVNGHSFLSDVPENIVASPSPYT
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98JP-0120551.
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98JP-0351246.
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66.6%;
                                                                                                                                                                                                           score 2860.5; DB 20;
Pred. No. 9.7e-262;
D9; Mismatches 132; I
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XX Soyb
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         18-DEC-1996;
                        18-DEC-1997;
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                                                                                        gastrointestinal flora; soybean
                                                                                                Raffinose synthetase; metabolism
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                                                                                                                                                                                                                        PIDSSSGGISVIEYLF 784
                                                                                                                                                                                                                                              FALYLYQAKKLILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPIGLVNMLNTSG
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                                                                                                                                                                 standard; Protein;
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          96JP-0338673
                         97EP-0122417
                                                                                                                                                                  781 AA
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Matches 525; Conserv
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Pred. No. 3.6e-261;
23; Mismatches 120; Indels 29;
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                                                                                                                                                                                                      Sequence
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18-DEC-1996;
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96JP-0338673
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01-SEP-1999;
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soybean plant promoters
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DB; AAC89523.
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| wp---sasklsmveflf 781
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Best Local Similarity
Matches 525; Conserv
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                                                       enykfrqycsgkds----ekgmgafvrdlkeqfrsveqvyvwhalcgywggvrpkvpgm
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             WPIDSSSGGISVIEYLF 784
                            TSGAIQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRACRIDGEDVGFKYDQDQMVVVQVP
                                                                                    IWNLNKFTGVIGAFNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIEWHSGENPISIEG
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sasklsmveflf
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                                                                                                                                                                                                                                                                                                                                                                                                             67.6%; Score 2854.5; DB 22; ilarity 65.9%; Pred. No. 3.6e-261; Conservative 123; Mismatches 120; I
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids and encoded proteins involved in the biosynthesis of raffinose, useful for producing soybean seeds with a reduced raffinose content and therefore improved nutritional quality -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-MAY-2000
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                                                                                                                                                                         ILEKSDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHAGD
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                                                dggcppgfvliddgwqcishdsdp-ekegmnqtvagegmpcrlisyeenykfrsy----
                                                                       DGGCPPGLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQMPCRLLKFQENYKFRDYVNPKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 47-49; 58pp;
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                                                                                                                                                                                                                    Novel mutant protein of raffinose synthase is useful raffinose oligosaccharide content in a plant body -
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DB; AAH27438.
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The present invention relates to a mutant protein of raffinose synthas in which at least one aromatic amino acid present at the position of about 1-7 amino acids from the N-terminus is deleted or replaced. The mutant protein can be used for reducing the raffinose oligosaccharide content in a plant body. The present protein from soybean, was used in the present invention.

Disclosure;

Page 18-20;

30pp;

Japanese.

synthase

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RESULT 1
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AC AAW5
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nes 526; Conserv
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                                                                         WPIDSSSGGISVIEYLF 784
                                                                                          TSGAIQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRACRIDGEDVGFKYDQDQMVVVQVP
                                                                                                             IWNLNKFTGVIGAFNCQGGGWCRETRRNQCFSQYSKRVTSKTNFKDIEWHSGENFISIEG
                                                                                                                                                                                                             DVIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISL
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Pred. No. 3.1e-259;
21; Mismatches 120;
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Best Local Similarity
Matches 508; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents the broad bean raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides in the host organism or cell is changed. Raffinose oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
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                                                                                                                                       KSP-----VSVGCFVGFDASEPDSRHVVSIGKLKDIRFMSIFRFKVWWTTHWVGRNGG 111
RVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVI
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RESULT 11
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          Query Match 65.9
Best Local Similarity 64.0
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                                                                    The present sequence represents a raffinose synthase protein. The sequence is isolated from plant material of broad beans. The protein forms raffinose by complexing alpha(1 to 6)- D-galactosyl hydroxyl group of the 6C of D-glucose residue in sucrose molecules
                                                                                                                  Claim 5;
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18-DEC-1996;
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96JP-0338673.
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EP849359-A2
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a; Japanese artichoke.
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Best Local Similarity
Matches 448; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is the Japanese artichoke raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides in the host organism or cell is changed. Raffinose oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              capable of producing raffinose, used as food beneficial effects on gastrointestinal flora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid molecule encoding plant raffinose synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                      wnynkftgvvgtfncqgggwsrevrrnqcaaeyshavsssagpsdiewkqgtspidvdgv
          WNLNKFTGVIGAFNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIEWHSGENPISIEGV
                                                  RAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGETMLKI 588
                                                                                                    rvgddfwctdpsgdpngtfwlqgchmvhcaynsiwmgnfihpdwdmfqsthpcaefhaas
                                                                                                                 RVGDDEWCTDPSGDPNGTFWLQGCHMVHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAAS
                                                                                                                                                        vihllemlcedyggrvdlakayykalsssvnnhfngngviaglehcndfmflgteaitlg
                                                                                                                                                                                   VIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLG
                                                                                                                                                                                                            eakliepkltpglkttmedlavdkivnngvglvppefveqmyeglhshlesvgidgvkvd
                                                                                                                                                                                                                         EARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKID 408
                                                                                                                                                                                                                                                             NYKFRDYVNPKATGPRAGQKGMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLP
                                                                                                                                                                                                                                                                                                                 \verb|phgvmegvqglvdggcppglvliddgwqsichdndalttegmgrtsageqmpcrlikfee|
                                                                                                                                                                                                                                                                                                                                PQGVIEGVRHLVDGGCPPGLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQMPCRLLKFQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1998-324670/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMITOMO CHEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 36-38; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96JP-0338673
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77.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 2529;
Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             food additives with
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.6e-230;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                            28-NOV-1997;
18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stachys sieboldii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY30144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY30144
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                             sequence
                                                                                                                                                                                                                                                                                                                        The present sequence
                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ10003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                           New raffinose synthase
                                                                                                                                                                                                                                                                                                                                                                                                         (SUMO ) SUMITOMO CHEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           649
                                                                                                             121
                                                                                                                                                                                                       109 NGGDLESETQIVILEKSDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDA
                                                                        181
                                                                                                                                                                   169
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                                                                                                                                229
                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              μ
                                                                                                                                                                                                                                                                                            e present sequence represents a raffinose synthase protein. The quence is isolated from plant material. The protein forms raffinose complexing alpha(1 to 6) - D-galactosyl hydroxyl group of the 6C D-glucose residue in sucrose molecules.
                                                                                                                                                                                      N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKID
                                                                       nykfreyespnktgp-gpntgmgafirdmkdnfksvdyvyvwhalcgywgglrpnvpglp
                                                                                                          ngsdleretqivvldksdd-rpyivllpliegqfraslqpgvddfidicvesgstkvnes
         VIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLG
                                  \verb"eakliepkltpglkttmedlavdkivnngvglvppefveqmyeglhshlesvgidgvkvd"
                                                                                 NYKFRDYVNPKATGPRAGOKGMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLP
                                                                                                                                                                                                                                                                                                                                                                                        1999-511112/43.
vihllemlcedyggrvdlakayykalsssvnnhfngngviaglehcndfmflgteaitlg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                         Page 30-31; 40pp;
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                            97JP-0329006
96JP-0338673
                                                                                                                                                                                                                                                                                                                                                                                                                                                        97JP-0342899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of a raffinose synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                     59.9%;
77.0%;
                                                                                                                                                                                                                                                                                                                                                                                                           CO LTD
                                                                                                                                                                                                                                                                                                                                                           gene - is prepared from
                                                                                                                                                                                                                           62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sucrose;
                                                                                                                                                                                                                          Score 2529; D. Pred. No. 1.6e 52; Mismatches
                                                                                                                                                                                                                                                                                                                                          Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA
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nes 70;
                                                                                                                                                                                                                                                DB
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                                                                                                                                                                                                                                                                                                                                                             plant material
                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                587;
                                                                                                                                                                                                                             2,
                                                                                                                                                                                                                             Gaps
                                                        408
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RRESULT 1
RAY32075
ID AAV3
XX AAV32075
AAC AAV3
XX AAV3
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Y M1sc
FT M1sc
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30-APR-1998;
04-DEC-1998;
10-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-
Misc-difference 132
This sequence represents rapessed raffinose synthase, a protein that can bind a D-galactosyl group through an alpha(1-6) bond to the hydroxy group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. cDNA (see AAZ20210) encoding the enzyme was isolated from rapessed cv. Wester leaf cDNA by PCR. Probes or primers generated from plant raffinose synthase genes (see AAZ20207-10) may be used to obtain
                                                                                                                                                                          Claim
                                                                                                                                                                                                               New sense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Raffinose synthase;
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                                                                                                                                                                                                                                                                                                                                                                                 (SUMO ) SUMITOMO CHEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALFTRDCLFEDPLHNGETMLKI 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RVGDDFWCTDPSGDPWGTFWLQGCHMVHCANDSLWWGNFIHPDWDMFQSTHPCAAFHAAS
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                                                                                                                                                                        27;
                                                                                                                                                                                                                                                                            AAZ20210
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                                                                                                                                                                   Page 36-38; 55pp; English
                                                                                                                                                                                                                 'n
                                                                                                                                                                                                                                                                                                                                         Oeda K;
                                                                                                                                                                                                             l antisense of food plants
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98JP-0120551.
98JP-0345590.
98JP-0351246.
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143
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144
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WO200024915-A2

Wheat raffinose synthase from

; raffinose synthase; wlm24.pk0021.hl; nut;

nutritional; soy protein

raffinose saccharide;

clone wlm24.pk0021.hl

09-AUG-2000

(first

entry)

AAY70980

standard;

Protein;

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RRESULT 1
AAY70980
ID AAY70987
XX AAY7
XX AAY7
XX OP-A
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                                                                                                                                                                                                                                 RACRIDGEDVGFKYDQDQMVVVQVPWPIDSSSGGISVIEYLF
                                                                                                                                                                                                                                                                               TVSPVTKLIQTSLHFAPIGLVNMLNTSGAIQSVDYDDDLSSVEIGVKGCGEMRVFASKKP
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73.9%;
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Pred. No. 6.7e-215;
71; Mismatches 71;
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Best Local Similarity
Matches 305; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids and encoded proteins involved in the biosynthesis of raffinose, useful for producing soybean seeds with a reduced raffinose content and therefore improved nutritional quality -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Allen
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DB; AAD00337.
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                                                         issvayntlflgefmqpdwdmfhslhpaaeyhgaaraiggcpiyvsdkpgnhnfdllkkl
                                                                                                                  svarnfpdngciscmchntdmly-sakqtavvrasddfyprdpas-----htvh
                                                                                                                                 SINKHFKGNGVIASMEHCNDFMFLGTEAISLGRVGDDFWCTDPSGDPNGTFWLQGCHMVH 496
                                                                                                                                                                          KVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVIHLLEMLCEDYGGRVDLAKAYYKAMTK 436
                                                                                                                                                                                                                                  ke-hgvksvyvwhamagywggvkpsaagmehyesalaypvqspgvtgnqpdivmdslsvl 352
                                                                                                                                                                                                                                                                                           sen----kedpsvavqegaqfasrltgikentkfqseqqeet-----pglkrlveetk 293
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|dcrfmclfrfklwwmtqrmgtsgrdvpletqfilievpaaagnddgdsepvylvmlplle 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dgr-lavrgrtvlsgvpdnvtaahasgaglvd----gafvgatageakshhvftfgtlr 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGSDFTVNGHSFLSDVPENIVASPSPYTSIDKSPVSVGCFVGFDASEPDSRHVVSIGKLK 87
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Search completed: November 30, 2001, 09:43:06 Job time: 165 sec

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Result
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Perfect score:
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Maximum DB seq length: 2000000000
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  Score
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Gapop 10.0 , Gapext 0.5
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YC47_SCHPO
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YCG2_RACT
FINCS_RACT
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PAGA_VIBCH
PARDE
ALN_YEAST
HMCS_HUMAN
HEMA_IAGRE
ALN_CAMJE
AGA1_PEDPE
NAC1_RACT
IMA1_XENTA
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014053 schizosacch
003745 bacillus th
0994k1 homo sapien
P45177 haemophilus
P197030 salmonalla
000156 ictalurid h
P51617 homo sapien
P55037 synechocyst
009435 caenorhabdi
P42242 bacillus su
P13217 drosophila
P17425 rattus norv
P22428 equine infe
P24019 vibrio chol
0029637 saccharomyc
P17293 paracoccus
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P17294 rattus norv
P17294 serratia ma
03840 thermotoga
P18311 synechocyst
P17247 equine infe
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SAMART; \$100030; WD40; 5. SMART; \$200030; WD40; 5. PROSITE; PS000678; WD_REPEATS_2; 2 PROSITE; PS50082; WD_REPEATS_REGI HYPOTHETICAL protein; Repeat; WD REPEAT 111 150 WD 2 REPEAT 158 198 WD 3 REPEAT 202 241 WD 3 REPEAT 243 283 WD 5 REPEAT 287 328 WD 5 REPEAT 33 376 WD 7 REPEAT 393 437 WD 8 REPEAT 570 611 WD 1 REPEAT 570 611 WD 1 REPEAT 570 611 WD 1 REPEAT 502 AA; 100569 MW; 5	RP SEQUENCE FROM N.A. RC STRAIN=972; RA Hilbert H., Duesterhoeft A., Wood V., Raja RA Hilbert H., Duesterhoeft A., Wood V., Raja RA Submitted (AUG-1998) to the EMBL/GenBank/ CC	SULT 1 47.SCHPO YC47_SCHPO STANDARD; 014053; 15.JUL-1998 (Rel. 36, Created) 15.JUL-1998 (Rel. 36, Last sec 20.AUG-2001 (Rel. 40, Last ann HYPOTHETICAL 100.6 KDA TRP-ASE CHROMOSOME III SPCC1672.07 Schizosaccharomyces pombe (Fis Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales; Schizosaccharomyces. NCBI_TaxID-4896; [1]	34 93 2.2 1047 1 ANPB_BOVIN 35 93 2.2 3988 1 POLG_BVIDVN 36 92.5 2.2 400 1 EFTU_HERAU 37 92.5 2.2 1356 1 HETI_PODAN 39 92.5 2.2 1356 1 HETI_PODAN 39 92.5 2.2 1431 1 DAPK_HUMAN 40 92 2.2 1431 1 DAPK_HUMAN 41 92 2.2 859 1 ENV_EIAVC 41 92 2.2 966 1 M172_HUMAN 42 92 2.2 1070 1 AGLU_CANTS 43 91.5 2.2 338 1 Y674_METJA 44 91.5 2.2 134 1 IF3X_HUMAN 45 91.5 2.2 1134 1 IF3X_HUMAN ALIGNMENTS
FC 1	d v.//GenBa EPEATS 	PRT; 902 AA. ated) t sequence update) t annotation update) t-ASP REPEATS CONTAINING PROTEIN C1672.07 IN (Fission yeast). (Fission yeast). ota; Schizosaccharomycetes; Schizosaccharomycetaceae;	B_BOVIN G_BVDVN P19711 bovine vira U_HERAU P19711 bovine vira U_HERAU P42477 herpetosiph P42477 herpetosiph P19701 influenza a 11_PODAN P19701 influenza a 200808 podospora a P53355 homo sapien P32541 equine infe P32541 equine infe P32541 equine sapien P32541 equine infe C2HUMAN P3355 homo sapien P39064 candida tsu U_CANTS P29064 candida tsu U_CANTS P29064 pendida tsu U_CANTS P29064 pendida tsu P3541 podospora P3541 equine infe

Query Match 2.7%; Score 115.5; D Best Local Similarity 20.0%; Pred. No. 0.31;

Matches 139;

Conservative

85;

Mismatches

DB 1; 1; 231;

Length 902; Indels 241;

Gaps

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RESULT

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SEQUENCE FROM N.A.

STRAIN-NRRL B-18457 / PS81A2;

Payne J.M., Sick A.J.;

Payne J.M., Sick A.J.;

Pagnes encoding lepidopteran-active toxins and transformed h

"Genes encoding lepidopteran-active toxins and transformed h

Patent number US5206166, 27-APR-1993.

-1- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO TH

-1- EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE.

-1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DUR

-1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DUR

-1- SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND
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Bacteria; Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Bacillus.
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                                                VPGTGSLWPLSVE-SPIGRCGEPNR--CVPHLEWNPDLDCSCRDGEKCAHHSHHFSLDID
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Matches 156
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EMBL; U83115; AAB53791.1;
HSSP; P02526; 1GAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ray M.E., Wistow G., Su Y.A., Meltzer P.S., Trent J.M.; "AIM1, a novel non-lens member of the betagamma-crystallin superfamily, is associated with the control of tumorigenicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000772; Ricin_B_lectin.
Pfam; PF00030; crystall; 6.
Pfam; PF00652; Ricin_B_lectin; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001064; Crystallin
InterPro; IPR000772; Ricin_B_lec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            malignant melanoma.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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   230
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hes 156;
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EUNCTION: MAY FUNCTION AS SUPPRESSOR OF MALICIANANT MELANOMA. EUURCTIONS MITH THE CYTOSKELETON EXERT ITS EFFECTS THROUGH INTERACTIONS MITH THE CYTOSKELETON SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY. CON'S TANDEM REPEATS OF A BETA/GAMMA-TYPE CRYSTALLIN DOMAIN.

SIMILARITY: CONTAINS 1 RICIN B-TYPE LECTIN DOMAIN.
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                                                                                                                                                                                                                                 VSFDGLNDMSSPFAIDGSDFTVNGHSFLSDVPENIVASPSPYTSIDKSPVSVGCFVGF-D 71
                                                                                                                                             IQDCSSWSLSPVILIKVVRGCWILYEQPNFEGHSIPLEEGELELSGLWGIEDILERHEEA 1102
                                                                                                                                                                                                     ISFSGMS-LSDTMTLRGS-------VQNKLNPRPGKVVIYSEPDVSEKCIEVFSD 1042
                            QGFGVMQKTCS-MKVHWGTWLIYEEPGFQGVPFILEPGEYPDLSFWDTEAAYIGSMRPLK 1206
                                                                                     ESDK-----PVVIGSIRHVVQDYRVSHIDLFTEPEGLGILSSYF------
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                                                         -- FALVKEAMKIVRTHLGTFRLLEEKTPPGI-----
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SM00247; XTALbg; 6.
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CRYSTALLIN BETA/GAMMA-LIKE 2.
CRYSTALLIN BETA/GAMMA-LIKE 3.
CRYSTALLIN BETA/GAMMA-LIKE 4.
CRYSTALLIN BETA/GAMMA-LIKE 5.
CRYSTALLIN BETA/GAMMA-LIKE 6.
RICIN B-TYPE LECTIN.
RICIN B-TYPE LECTIN.
                                                                                                                                                                                                                                                            Score 106; DB
Pred. No. 4.8;
27; Mismatches
                                                                                                                                                                                                                                                                                                                                    MW;
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                                                          -VDKFGWCTWDAFYLTVHP--
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P45177;
01-NOV-1995
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                                                                         SEQUENCE FROM N.A.

STRAIN-RD / KW20 / ATCC 51907;

MEDLINE-95350630; PubMed-7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKerney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weldman J.F., Phillips C.A., Spriggs T., Heblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLGB
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01-NOV-1995 (Rel. 32, Last
20-AUG-2001 (Rel. 40, Last
1,4-ALPHA-GLUCAN BRANCHING
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Bacteria; Proteobacteria;
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"Whole-genome influenzae Rd.
                                                        Venter J.C.;
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-!- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycogen biosynthesis; Transferase; Glycosyltransferase;
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KNOWN AS THE ALPHA-AMYLASE FAMILY.
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                             VLPDGSILRSEYYALPTRDCLFEDPLHN-----GETMLKIWNLNKFTGVIGAF---
                                                                                     MVHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKL
                                                                                                                  TNWKI--HSEMAGAISIAEESTSFAGV-THPSENGGLGFNE
                                                                                                                                              MTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLGRVGDDFWCTDPSGDPNGTFWLQGCH 493
                                                                                                                                                                            VKNFLSSNALYWLERFGVDGIRVDAVASMIYRDYSRAEGEWIPNQYGGRENLEAIEFLKH
                                                                                                                                                                                                                                     ------GL-----VAFDGTALY-----EHEDPREGYHQDWNTLIYNYGRNE
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                                                                                                                                                                                                                                                                                                                                                      HIEFLPLSEFPFDGSW------GYQPLGLYS-PTSRFGSPEAFR-----RLVK---
                                                                                                                                                                                                                                                                                                                                                                                  HL-----VDGGCPPGLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQMPCRLLKFQE
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 SENFVLPLS - - - HDEVVHGKYSLLGKMPGDTWQKFANLRAYYGYMWGYPGK
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HEMA_IARUD
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01-FEB-1991 (Rel. 17, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
HEMAGGLUTININ HA2 CHAIN].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
PRINTS; PR00329; HEMAGGLUTN12.
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HSSP; P03437; 2HMG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
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ProDom; PD000225; Hemagglutn;
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Influenza virus A and B group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Influenza A virus (strain A/Ruddy Turnstone/New Jersey/47/85).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 630
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                                                                                                                                                                                                                                                                                  NGGSNVVSFDGLND-----MSSPFAIDGSDFTVNGHSFLSDVPENIVASPSPYTSIDKS
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                                            VNNGDYARLY IWGVHHPSTDTEQTNLYKNNPGRVTVSTKTSQTSVVPNIGSRPLVRGQSG
                                                                                                                                     LANNGKF-EFIAEEFQWNTVKQNGKSGACKRANVNDFFR-RLNWLTKSDGNAYPLQNLTK
                                                                                                                                                                                                                                     NGALGSPGCDHLNGAEWDVFIERPTAVD-----
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-FRTSIQPGD--
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N-LINKED (GLCNAC. . . ) (PO)
N-LINKED (GLCNAC. . . ) (PO)
                                                                                                                                                                                                                                                                                                                                                       Score 102.5;
Pred. No. 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEMAGGLUTININ HA1 CHAIN.
HEMAGGLUTININ HA2 CHAIN.
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rus H4 hemagglutinin
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DDFVDVCVESGSS
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RESULT 6
RFBK_SALCH
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Q00330;
Q1-QCT-1994 (Rel. 30, Created)
Q1-QCT-1994 (Rel. 30, Last sequence update)
Q1-QCT-1994 (Rel. 40, Last annotation update)
Q1-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                        Brown P.K., Romana L.K., Reeves P.R.;
"Molecular analysis of the rfb gene cluster muenchen (gtrain M67): the genetic basis of groups C2 and B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella cholerae-suis (Salmonella enterica).
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92349966; PubMed=1379320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                              Pfam; PF00408; PGM_PMM; 1. PROSITE; PS00710; PGM_PMM; 1.
                                                                              EMBL; X61917; CAA439;
PIR; S22622; S22622.
                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                 modified and this statement is not removed.
                                                                 InterPro;
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            ipopolysaccharide biosynthesis;
                                                                                                                                                                                                                                                                                   MICTODIOI. 6:1385-1394(1992).

FUNCTION: INVOLVED IN GDP-MANNOSE BIOSYNTHESIS WHICH SERVES AS THE ACTIVATED SUGAR NUCLEOTIDE PRECURSOR FOR MANNOSE RESIDUES IN CELL SURFACE POLYSACCHARIDES. THIS ENZYME PARTICIPATES IN SYNTHESIS OF THE LPS GROUP C2 O ANTIGEN.

CATALYTIC ACTIVITY: D-MANNOSE 1-PHOSPHATE - D-MANNOSE 6-PHOSPHATE.

PATHWAY: GDP-MANNOSE BIOSYNTHESIS.
                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE PHOSPHOHEXOSE MUTASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNDFMFLGTEAISLGRVGDDFWCTDPSGDPNGTFWLQGCHMVHCAND-SLWM 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --IDGWYGFR-HQNAEGTGTAADLKSTQAAIDQINGKLNRL---------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNNCI---ESIRNGTYDHDIYRDEAI---NNRFQIQGVKLTQGYKDIILWI 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DTKIDLWSYNAELLVALENQH--TIDVTDSEMNKLFERVRRQLRENAEDKGNGCFEIFHQ
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                                                              IPR001485; PGM_PMM.
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                Isomerase;
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the polymorph
              Transmembrane;
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VG64_HSVI1 STANDARD; 'PRT; 514 AA.

ID VG64_HSVI1 STANDARD; 'PRT; 514 AA.

AC Q00156;
DT Q1-DEC-1992 (Rel. 24, Last sequence update)
DT Q1-DEC-1992 (Rel. 24, Last annotation update)
OC Viruses; dsDNA viruse; nc RNA stage; Herpesvirus
CX Unclassified Herpesviridae.
OX NCBI_TRAID-10401;
RN G12-DAVID N.A.
STRAIN-AUBURN 1;
RN MEDLINE-92087490; PubMed-1727613;
RN MEDLINE-92087490; PubMed
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                                                                          Matches 108;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ictalurid herpesvirus 1 (Channel catfish virus) (CCV Viruses; dsDNA viruses, no RNA stage; Herpesviridae, unclassified Herpesviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323
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TVNGHSFLSDVPENIVASPSPYTSIDKSPVSVGCFVG-----FDASEPDSRHVVSI 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKLVLPDGSILRSEYY-----ALPTRDCL 574
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21.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a new type of herpesvirus.";
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                                                                             75;
                                                                                                   Score 101; DB Pred. No. 2.1;
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POTENTIAL.
FORMS THE PHOSPHOSERINE INTERMEDIATE
(BY SIMILARITY).
982E5B885083B893 CRC64;
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Pred. No. 1.
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                                                                                                                   SEQUENCE FROM N.A.

Reichwald K., Kioschis P., Rosenthal A., Platzer M.;

Reichwald K., Kioschis P., Rosenthal A., Platzer M.;

Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: INVOLVED IN IL-1 PATHWAY. THIS KINASE ASSOCIATES

THE IL-1 RECEPTOR IL1-R-1. THIS ASSOCIATION IS RAPID AND II
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., I
MEDLINE=96180673; Pul
Cao Z., Henzel W.J.,
                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
INTERLEUKIN-1 RECEPTOR-ASSOCIATED KINASE 1
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                       ACTIVATION OF THE KINASE SIMILARITY: BELONGS TO THE
                                                SMALL AMOUNTS.

PTM: AN EXTENSIVE PHOSPHORYLATION
ASSOCIATION WITH ILL-R-1. THIS STI
                                                                                            TISSUE SPECIFICITY:
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                                                                                                                                                                                                                                                          271:1128-1131(1996).
                                                                                                                                                                                                                                                                       Henzel W.J., Gao X.;
kinase associated with the interleukin-1 receptor.";
                                                                                                                                                                                                    (MAR-1995)
            SUBFAMILY
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                                                                                                                                                                                                                  Drescher B.;
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inactivation or a
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EMBL; U52112; AAC51752.1; -.
EMBL; AF030876; AAC08756.1; -.
EMBL; AF031075; AAF21636.1; -.
                                                                                                                                                                     Navarro F., Chavez S., Candau P., Florencio F.J.; "Existence of two ferredoxin-glutamate synthases cyanobacterium Synechocystis sp. PCC 6803. Isolatinactivation of gltB and gltS genes."; plant Mol. Biol. 27:753-767(1995).
          SEQUENCE FROM N.A.

MEDLINE-97061201; PubMed-8905231;

Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
                                                                                                                                                                                                                                                                                                                                                                          Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales;
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLTB OR SLL1502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLTB_SYNY3 STANDARD; PRT; 1550 AA P55037; P55037; O1-OCT-1996 (Rel. 34, Created) O1-OCT-1996 (Rel. 34, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation updat FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE 1 (
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InterPro; IPR002965; P_rich_extensn.
InterPro; IPR002990; Ser_thr_kin_actsite.
pfam: pF00069; pkinase; 2.
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212 521 PROTEIN KINASE.
218 226 ATP (BY SIMILARITY).
239 239 ATP (BY SIMILARITY).
338 338 BY SIMILARITY.
338 38 BY SIMILARITY.
319 196 19 F -> S (IN REF. 1).
532 532 S -> L (IN REF. 1).
532 532 S -> L (IN REF. 1).
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EMBL; D90992; BAA17018.1; -.
HSSP; P02392; ICTF.
InterPro; IPR002489; DUF14.
InterPro; IPR002932; Glu_synthase.
Pfam; PF01493; DUF14; I.
Pfam; PF01493; DUF14; I.
Oxidoreductase; Iron-sulfur; 3Fe-45;
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CATALYTIC ACTIVITY: 2 L-GLUTAMATE + 2 OXIDIZED FERREDOXIN -
L-GLUTAMINE + 2-OXOGLUTARATE + 2 REDUCED FERREDOXIN.
COFACTOR: BINDS A 3FE-4S CLUSTER, FAD AND FMN.
COFACTOR: BINDS A 3FE-4S CLUSTER, FAD AND FMN.
PATHWAY: GLUTAMINE SYNTHENASE/COGAT PATHWAY WHICH IS INVOLVE
IN THE ASSIMILATION OF AMMONIA.
SIMILARITY: TO OTHER GLUTAMATE SYNTHASES.
CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-21 IS THE INIT
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ctase; Iron-sulfur; 3Fe-45; Flavoprotein; FAD; FMN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sugiura M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
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Sugiura M., Tabata S.
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SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
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                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00452; GUANYLATE_CYCLASES_1; PROSITE; PS50125; GUANYLATE_CYCLASES_2; PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                DFWCTDPSGDPNGTFWLQGCHMVHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAASR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APSISTGHSGVTTV------SDFCEN-YTMMMYEKEMVLTAKYQYTHLTKAD
                                                                                                                                           ---KELTLEKKKAD-ILLSR--MLPKQVAERLKAG--QTVEPEGFDSVTVFFSDVVKFTI
                                                                                                                                                                                                                                                                                                                                                                                                                                          KERFVKMRKLDHENINRFIGLSI - - - DSAHFISVTKL - - -
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NVELRIGVNSGPC-VAGVVG
                                              GYLCVSGLPTRNGY ----AHIKQIVDMSLKFMEY
                                                                                                                     LEMLCEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLGRVGD
                                                                                                                                                                    SPGLOMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKI---DVIH--L
                                                                                                                                                                                             PTAENICSQMKGLVS----KQKTNLMDHVF--NMLEEYTSTLEEEI---
                                                                                                                                                                                                                   PKATGPRAGQKGMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLPEARVIQPVL
                                                                                                                                                                                                                                           TDIHDVNPALIALVKDCWAEVPED-----
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                                                                                                                                                                                                                                                                                                                                           HKTFLRLHGNLRSATCLVNDSWQVKLAEYGMDNLVEEQTPPKKRLLWVAPEVLRGSLSVS
                                                                                                                                                                                                                                                                                                                                                                  FRSMLYLHAG-DDPFALVKEAMKIVRTHLGTFRLLEEKTPPG---
                                                                                                                                                                                                                                                                                                                                                                                          RGSLQD-----CIIRDVAKGLEYL 674
                                                                                              LASKCSPF-QTVNLLNDLYSNFDTIIEQH----GV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                        ·AISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGE
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pkinase; 2.
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17.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78;
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GUANYLATE CYCLASE.

N-LINKED (GLCNAC. .) (POTENTIAL).

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Pred. No. 9.7;
78; Mismatches
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9.7;
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Best Local Similarity
Matches 54; Conserv
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15-JUL-1999 (Rel. 3
20-AUG-2001 (Rel. 4
HYPOTHETICAL 34.5 K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus/Staphylococcus group; Bacillus. Recillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YCBJ_BACSU
P42242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-I-SIMILARITY: TO AMINOGLYCOSIDE PHOSPHOTRANSFERASES AN
TO VIOMYCIN PHOSPHOTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D30808; BAA06474.1; -. EMBL; 299105; CAB12046.1; -. Subtilist; BG11165; ycbJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ogawa K.-I., Akagawa E., Nakamura K., Yamane K.; "Determination of a 21548 bp nucleotide sequence around degrees region of the Bacillus subtilis chromosome."; Microbiology 141:269-275(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-95219079; PubMed-7704254; Ogawa K.-I., Akagawa E., Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-168;
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Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Transferase; Kinase;
                                                                                                                                182
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                                IHGDLHPPHILIDQNGRVTGLLDWTEAKVADPAKDFVLYQTIFGEKETARLLEYYDQ---
                                                                                              QISAGQSGIEVIRPE--DFRQMTADSMVDVKNKLGVSTTLWERWQKWVDDDAYWPGFSSL
                                                                                                                           PFALVKEAMKIVRTHLGTFRLLEEKTPPGIVDKFGWCT--WDAFYLTVHPQGVIEGVRHL
                                                                                                                                                                                                                                                      VILEKSDSGRPYV------LPIV 138
   RDYVNPKATGPRAGQKGMKAFIDELKGEF 321
                                                               VDGGCPPGLVLIDDGWQSIG------HDSDPITKEGMNQTVAGEQMPCRLLKFQENYKF
                                                                                                                                                            KGTPAAGIDLEQKQYVWNMDHQPPSDDFVRTLADILAE
                                                                                                                                                                                                                          VVFAKDDTGMPWVLRKPRRSDVVERASAEGITLAFLRANLTADVPDWRIHTPELIAYPML
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306 AA;
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38,
40,
KDA
                                                                                                                                                                                                                                                                                                                                                               204 BY SIMILARITY.
34481 MW; 5EF0FD9EC085977D CRC64;
                                                                                                                                                                                                                                                                                                  2.3%; Score 98; DB 1;
20.1%; Pred. No. 1.7;
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Last annotation update)
PROTEIN IN GLTP-CWLJ IN
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                                                                                                                                                                                           QPGDDDFV----DVCVESGSSKVVDASFRSMLYLHAGDD 181
                                                                                                                                                                                                                                                                                   33; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                               ATP-binding;
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                                                                                                                                                                                                                                                                                                                  Length 306;
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ALD DOOR RESERVE TO THE TENERS OF THE TENENS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
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P13217;
01-JAN-1990
      DOMAIN
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                    SMART;
                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00168; C2; 1.
Pfam; PF00388; PI-PLC-X; 1.
Pfam; PF00387; PI-PLC-Y; 1.
PRINTS; PR00390; PHPHLIPASEC.
PRODOM; PD001202; PI_PLC_Y; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Bloomquist B.T., Shortridge R.D., Schneuwly S.,
Montell C., Steller H., Rubin G., Pak W.L.;
"Isolation of a putative phospholipase C gene of
and its role in phototransduction.";
Cell 54:723-733(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EC
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01-NOV-1995 (Rel. 32, Last sequence update)
01-CT-1996 (Rel. 34, Last annotation update)
1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE
                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                 SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR000008; C2.
Interpro; IPR001192; PI_PLC.
Interpro; IPR000909; PI_PLC_X.
Interpro; IPR001711; PI_PLC_Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A31225; A31225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J03138; AAA28724.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; FBgn0004625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P10688; 1QAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rities requires a license agreement (See http://www.isb-sib.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C ENZYMES. NORPA IS INVOLVED IN PHOTOTRANSDUCTION.
CATALTYIC ACTIVITY: 1-PHOSPHATIDYL-D-MYO-INOSITOL 4,5-BISPHOSPHATE
+ H(2)O = D-MYO-INOSITOL 1,4,5-TRIPHOSPHATE + DIACYGLYCEROL.
SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
SIMILARITY: CONTAINS 1 C2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.1.4.11) (PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE
E; PS50004; C2_DOMAIN_2; 1.
E; PS50008; PIPLC_X_DOMAIN; T.
Ase; Lip1d degradation; Vision; T.
Ase; Lip1d degradation; Vision; T.
Ase; Lip1d degradation; Vision; T.
Ase; DOMAIN X.
C2 DOMAIN X.
C2 DOMAIN Y.
C2 DOMAIN Y.
C3 34 34 BY SIMILAR
TE 381 381 BY SIMILAR
TE 381 381 BY SIMILAR
                                                                                                                                                                                                                                                                                                                    SM00239; C2; 1.
SM00148; PLCXC; 1.
SM00149; PLCYC; 1.
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   DOMAIN X.
DOMAIN Y.
C2 DOMIN.
C2 DOMIARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
C2 MW; 2D945EF0ACBE69B3 CRC64;
                                                                                                                                                                                                Transducer
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Query Match Best Local Similarity

2.3%;

Score 97.5; Pred. No. 12;

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Gil G., Goldstein J.L., Slaughter C.A., Brown M.S.;
"Cytoplasmic 3-hydroxy-3-methylglutaryl coenzyme A synthase from the
hamster. I. Isolation and sequencing of a full-length cDNA.";
J. Biol. Chem. 261:3710-3716(1986).

-i- FUNCTION: THIS ENZYME CONNDENSES ACETYL-COA WITH ACETOACETYL-COA
TO FORM HMG-COA, WHICH IS THE SUBSTRATE FOR HMG-COA REDUCTASE.

-i- CATALYTIC ACTIVITY: (S)-3-HYDROXY-3-METHYLGLUTARYL-COA + COA =
ACETYL-COA + H(2)O + ACETOACETYL-COA.

-i- PATHWAY: PRODUCTION OF MEVALONATE FROM HMG-COA PRIOR TO THE
SYNTHESIS OF STEROLS SUCH AS CHOLESTEROL AND ISOPRENOIDS.

-i- SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                     01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-1996 (Rel. 34, Last annottation update)
HYDROXYMETHYLGLUTARYL-COA SYNTHASE, CYTOPLASMIC (EC 4.1.3.5) (HMG-COA SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         HMCS_
                                                                                                                                                                                      TISSUE=Ovary;
MEDLINE=86140166; PubMed=2869035;
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      NCBI_TaxID=10029;
                                                                                                                                                                                                                                                                    Cricetulus
                                                                                                                                                                                                                                                                                                                                         HMGCS1 OR HMGCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEDPFVFRKVVLPDLAVLRFGVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>APVDGVIAAQCSVKVIAGQFLSDKKVGTYVEVDMFGLPSDTVKKEFRTRLVANNGLNPVY</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NYMPQVFWNAGCQMVSLNFQSSDLPMQLNQGKFEYNGGCGYLLKPDFMRRADKDFDPFAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVDLAKAYYKAMTKSINKHFKGNGVIASMEHC--NDFMFLGTEAISLGRVGDDFWCTDPS
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          HMCS_RAT
P17425;
01-AUG-1990
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01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
HYDROXYMETHYLGLUTARYL-COA SYNTHASE, CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01226; HMG_COA_SYNTHASE; 1.
Lyase; Cholesterol biosynthesis; Multigene family.
ACT_SITE 129 129 POTENVIAL.
SEQUENCE 520 AA; 57318 MW; 2D4CAAE7DEE5D6BB CF
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PIR;
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L00330; AAA37076.1;
L00331; AAA37076.1;
L00332; AAA37076.1;
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                                                                                                                                   DRDVEK
                                                                                                                                                            KYDQDQ 760
                                                                                                                                                                                    L--ARMFLNDFLN---
                                                                                                                                                                                                             LHFAPIGLVNMLNTSGAIQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRACRIDGEDVGF
                                                                                                                                                                                                                                                             EWHSGENPISIEGVKTFALYLYQAKKLILSKPSQDLDIALDPFEFELITVSPVTKLIQTS
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L00327;
L00328;
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                                                                                                                                                                                                                                                                                                                    FEDPLHNGETMLKIWNLNKFTGVIGAENCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pro; IPR000590; HMG_COA_synt.
PF01154; HMG_COA_synt; 1.
TE; PS01226; HMG_COA_SYNTHASE;
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AAA37076.1;
AAA37076.1;
AAA37076.1;
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    4.1.3.5) (HMG-COA
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X52625; CAA36852.1;

PIR; S12736; S12736.

InterPro; IPR000590; HMG_COA_synt.

Pfam; PF01154; HMG_COA_synt; 1.

PROSITE; PS01226; HMG_COA_SYNTHASE; 1.

Lyase; Cholesterol blosynthesis; Multigene family.

ACT_SITE 129 129 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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HMGCS1 OR HMGCS.
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                                              696 HFAPIGLYNMLNTSGAIQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRACRIDGEDVGFK 755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     378 VGLVPPE------KAE-EMYEGLHAHLEKVGIDGVKIDVIHLLEMLCEDYGGRVDLA 427
276
                                                                                                                                                                                                                  214 -- PVVDGKLSIQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 VGTVALETYFPSQYVDQAELEKYDGVDAGKYTTGLGQARMG-----FCTD---REDIN 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSGDP-----NGTFWLQGCHMVHCANDSLWMGNF---IHPDWDMFQS--THP 520
--ARMFLNDFLN------EDTYFD
                                                                                                                                                           WHSGENPISIEGVKTFALYLYQAKKLILSKPSQDLDIALDPFEFELITVSPVTKLIQTSL 695
                                                                                                                                                                                                                                                                        EDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIE 635
                                                                                                                                                                                                                                                                                                                               TGGVGAVALLIGPNAPVIFDRGLRGTHMQHAYDFYK----PD---MLSEY-----
                                                                                                                                                                                                                                                                                                                                                                                   CAAFHAASRAISGGPIYVSD-----SVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLF 575
                                                                                                                                                                                                                                                                                                                                                                                                                                            IEGIDTTNACYGGTAAVFNAVNWIE-----SSSWDGRYALVVAGDIAIYASGNARP 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLCLTVVQKLMERNSLSYDCIGRLE-----VGTETIIDKSKSVKSNLMQLFEESGNTD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAI-----SLGRVGDDFWCTD 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57433 MW; CB213A27B0C177CB CRC64;
                                                                                                                                                                                                                  -QKEGKDKDFTLNDFGF-MIFHSPYCKLVQKSL
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313 RDVEK 317
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Search completed: November 30, 2001, 09:41:02 Job time: 41:sec

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Run
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Listing first 45 summaries
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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       seq length: 0
seq length: 2000000000
                                                                                           Match
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1: /cgn2_6/ptodata/2
2: /cgn2_6/ptodata/2
3: /cgn2_6/ptodata/2
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/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
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US-08-846-234-5
US-08-770-544-2
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US-08-251-645-6
US-08-291-368-2
US-08-962-190-2
PCT-US95-10310-2
$164180-4
US-08-305-505-6
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-846-234-5
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; Patent No. 6166292
                                                                                                                              TELEPHONE: (703)-413-
TELEFAX: (703)-413-22
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: OSUMI CIACONA APPLICANT: NOZAKI Jinshi APPLICANT: KIDA Takao APPLICANT: KIDA Takao TITLE OF INVENTION: PRODUCING RAFFINOSE, AND TITLE OF INVENTION: PRODUCING RAFFINOSE, AND TITLE OF GROUENCES: 22
                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 784 amino acids
TYPE: amino acid
                                                                                                                                                                                           REGISTRATION NUMBER: 24,618 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,234
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1755 S.
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
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                                                                                                                            E: (703)-413-3000
(703)-413-2220
FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OBLON, SPIVAK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
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TRANSGENIC
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Query Match 100.0%; Score 4225; Best Local Similarity 100.0%; Pred. No. 0; Matches 784; Conservative 0; Mismatches

DB

784; 0;

0;

Indels Length

Gaps

0,

61 PVSVGCFVGFDASEPDSRHVVSIGKLKDIRFMSIFRFKVWWTTHWVGRNGGDLESETQIV 120

1 MAPSFKNGGSNVVSFDGINDMSSPFAIDGSDFTVNGHSFISDVPENIVASPSPYTSIDKS 60 MAPSFKNGGSNVVSFDGLNDMSSPFAIDGSDFTVNGHSFLSDVPENIVASPSPYTSIDKS 60

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US-08-846-234-1
                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08846234 Patent No. 6166292
                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                            TITLE OF INVENTION: RAFFINOSE TITLE OF INVENTION: PRODUCING
                                                                                                                                                                                                                          APPLICANT: NOZAKI Jinshi
APPLICANT: KIDA Takao
                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                  COUNTRY: US
ZIP: 22202
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                                                                                                                                                                                                                                                                                                                                                                                                        781 EYLF 784
                                                                                    STREET: 1755 S. CITY: ARLINGTON STATE: VIRGINIA
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                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGETMLKIWNLNKFTGVIGA 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPFALVKEAMKIVRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVHPQGVIEGVRHLV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                          EYLF 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSSVEIGVKGCGEMRVFASKKPRACRIDGEDVGFKYDQDQMVVVQVPWPIDSSSGGISVI 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPIGLVNMLNTSGAIQSVDYDDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPIGLVNMLNTSGAIQSVDYDDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDPNGTFWLQGCHMVHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYVSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLGRVGDDFWCTDPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLGRVGDDFWCTDPS 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVIHLLEMLCEDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVIHLLEMLCEDY 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGPRAGQKGMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLPEARVIQPVLSPG
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                                                                                                                       E: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                      USA
                                                                                                                                                                                                                                                                  OSUMI Chieko
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                                                                                                                                                                                            SYNTHASE GENE, RAFFINOSE, AND
                                                                                                                                                                                             METHOD FOR TRANSGENIC
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; FRAGMENT TYPE:
US-08-846-234-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-D
SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
         MOLECULE TYPE:
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                       STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                 NAME: Goldman, Michare REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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Query Match 4.3%;
Best Local Similarity 100.0%;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-413-3000
TELEFAX: (703)-413-2220
INFORMATION FOR SEQ ID NO: 1:
             TELEPHONE: (716) 263-1304
TELEPAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600
FILING DATE: 21-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: NORMAN F. OBLON
                                                                 REFERENCE/DOCKET NUMBER: 19603/621
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gonsalves, Dennis APPLICANT: Ling, Kai-Shu
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5. 5907085
                                                                                                                                               Goldman, Michael
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Clinton Square,
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In Release #1.0, Version #1.30 (EPO)
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quare, P.O. Box 1051
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GENERAL INFORMATION:
APPLICANT: Kramer, Vance C.
APPLICANT: Morgan, Michael K.
APPLICANT: Morgan, Michael K.
APPLICANT: Morgan, Arne R.
APPLICANT: Hart, Hope
APPLICANT: Warren, Gregory W.
APPLICANT: Dunn, Martha
APPLICANT: Dunn, Martha
APPLICANT: Chen, Jeng S.
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: AND NUCLEIC ACID SEQUENCES CODING THEREFOR
FILE REFERENCE: CGC1963/A
CURRENT APPLICATION NUMBER: US/09/251,645
CURRENT FILING DATE: 1999-02-17
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Best Local Similarity
Matches 137; Conserv
                                                                                                                                                                                                                     Sequence 6, Application US/09251645 Patent No. 6281413
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20.6%; Pred. No. 0.11;
ative 78; Mismatches 233; Indels 21
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; TYPE: PRT
; ORGANIZM: Photorhabdus luminescens
US-09-251-645-6
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 6
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Query Match 2.5%; Score 107.5; Best Local Similarity 18.5%; Pred. No. 0.2; Matches 186; Conservative 132; Mismatches
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                                                                    6 KNGGSNVVSFDGLNDMSSPFAI---DGS--DFTVNGHSFLSDVPENIVA-----SPS 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVLGQLSKEISNDWLWNLSANPLVRLATPLVTTKTYKYDGWGNLYSTEYSDGRIELEIHD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIQTNTSREETVNIKSDDWGNTLLITETSGIQKEYVYYPVNGEGNSCPADPLGFS---RF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDENDFWPVMIEVDSQGVRRKTHYDGMGRICSIEEQDDDGAWGTSGIYQGTYRKVLARQY 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKSVTQKGS-PDAAQSVANKVIHYTYQKFPTFTGAYV-----KEYVSKVSETID 501
-VGGRKTEYLYGPQGDKPIQSITPSHNKQNMDYLYYLGSVMSKFTTGTDQQNFRYHSKTG
                                                                                                                                                                                                                             MLKIWNLNKFTGV-IGAFNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIEWHSGENPI
                                                                                                                                                                                                                                                                                                                                                                                 HAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGET 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AHMESKNVTSIYTHRQLRKVDVNHVITDQSYDLLGRITGQIIDPGTAREIKRNYVYQYPG 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AHLEKVGIDGV-----KIDVIHLLEMLCEDYGGRV-------
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US-08-040-751-3
Sequence 3, Application US/08040751
Patent No. 5407825
GENERAL INFORMATION:
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; LIBRARY: Lambda
; CLONE: 81A2
US-08-040-751-3
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                                                                                                                                                                         Query Match 2.5%; Score 107; DB 1; I Best Local Similarity 19.6%; Pred. No. 0.14; Matches 111; Conservative 82; Mismatches 181;
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SEQUENCE CHARACTERISTICS:
LENGTH: 1174 amino acids
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TOPOLOGY: linear
MOLECULE TYPE: prot
HYPOTHETICAL: YES
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NAME: SALIWANCHIK, DAVID R.
REFERENCE/POCKET NUMBER: MA39.C1.D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
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APPLICATION NUMBER: US
FILING DATE: 19930329
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APPLICANT: Sick, August J
TITLE OF INVENTION: No. 5407825el Bacillus thuringiensis isolates
TITLE OF INVENTION: active against Lepidopteran Pests and Genes Encoding No. 54078
TITLE OF INVENTION: Lepidopteran-active Toxins
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: YI
ANTI-SENSE: NO
ORIGINAL SOURCE:
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                           373 I-----VLHKVGLVPPEKAEEMY--EGLHAHLEKVGIDGVK--IDVIHLLEMLCEDYG 421
                                                                                 314 YWAGHRVTSHFTGSSQVISSPQYGITANAEPSRTIAPSTEPGLNLFYRTLSDPFFRRSDN 373
374 IMPTLGINVVQGVGFIQPNNGEVLYRRRGTVDSLDELPIDGENSLVGYSHRL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DAVID R. SALIWANCHIK
STREET: 2421 N.W. 41st STREET, SUITE A-1
CITY: GAINESVILLE
STATE: PT
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                STRAIN: aizawai
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USA
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linear
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                                                                                                                                                                                                2.5%; Score 107; DB 1; Length 1174; 19.6%; Pred. No. 0.14;
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    425
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US-089-1 PARESULT	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
ULT 6 08-291-368-2 108-291-368-2 leaguence 2, Application US/08291368 atent No. 5686069 general Information: APPLICANT: Sayne, Jewel M. APPLICANT: Stok, August J. APPLICANT: Jake Active Against Lepidopteran Pests NUMBER OF SEQUENCES: 27 CORRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville STATE: FL COUNTRY: US ZIP: 33606 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/291,368 FILING DATE: 15-OCT-90 FILING DATE: 15-OCT-90 CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: 07/597,607 FILING DATE: 15-OCT-90 CLASSIFICATION SAIWANCER: MA50.Cl TELEFAX: (904)375-8800 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:	422 GRVDLAKAYYKAMTKSI

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US-08-962-190-2

; Sequence 2, Application US/08962190

; Patcent NO. 5985267

; Patcent NO. 5985267

; APPLICANT: Payne, Jewel M.

; APPLICANT: Sick, August J.

; TITLE OF INVENTION: NO. 5985267el Bacillus thuringiensis

; TITLE OF INVENTION: Active Against Lepidopteran Pests

; NUMBER OF SEQUENCES: 27
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; CLONE: 81A2
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Best Local Similarity
Matches 111; Conserv
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INDIVIDUAL ISOLATE: PS81A2
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                    728 VKGCGEMRVFASKKPRACRIDGEDVG 753
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                                                                                                                                                                                                                                                                                                       VPGTGSLWPLSVE-SPIGRCGEPNR--CVPHLEWNPDLDCSCRDGEKCAHHSHHFSLDID 824
                                                                                                                                                                                                                                                                                                                                                                                                            PISIEGV--KTFALYLYQAKKLILSK----
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19.6%; Pred. No. 0.14;
ative 82; Mismatches 181; Indels 192;
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                                                        Isolates
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US-08-962-190-2
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APPLICATION NUMBER: U
FILING DATE:
APPLICATION NUMBER:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 1174 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (904)375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
ORGANISM: Bac
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
596 IPVDATFEAEYDLERAQKAVNSLFTS---SNQIELKTDVTDYHIDQVSNLV---DCLSDE 649
                                 555 LPDGSILRSEY---YALPTRDCLFEDPLHNGETMLKI----WNLNKFTGVIGAFNCQGGG 607
                                                                                                                                                                                                                                                                                                                                                                      314 YWAGHRVTSHFTGSSQVISSPQYGITANAEPSRTIAPSTFPGLNLFYRTLSDPFFRRSDN 373
                                                                                                                                                                                                                                                                                                                                                                                                           336 YWGGLR------PQVPGLPE------ARVIQPVLSPGLQMTMEDLA-----VDK 372
                                                                        546 TMSANGSLTSQSFRFAEFPVGIST-----SGSQTAG-ISISNNPGRQTFHLDRIEF
                                                                                                                                                                                   469 RVGDDFWCTDPSGD-----
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 2.5%; Score 107; DB Local Similarity 19.6%; Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN: aizawai INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA50.C1
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                                                                                                                                                                                                                                                                                                                        I------VLHKVGLVPPEKAEEMY--EGLHAHLEKVGIDGVK--IDVIHLLEMLCEDYG 421
                                                                                                         VHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLV 554
                                                                                                                                              FTGGDIIRTNVNGNVLSMSLNFSNTSLQRYRVRVRYAASQTMVMRVNVGGSTTFDQGFPS
                                                                                                                                                                                                                      SHVTLTRSLYNTNITSLPTFVWTHHSATDRNIIYPDVITQIPLVKSFSLTSGTSVVRGPG
                                                                                                                                                                                                                                                                                              IMPTLGINVVQGVGFIQPNNGEVLYRRRGTVDSLDELPIDGENSLVGYSHRL-----
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GENERAL INFORMATION:
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APPLICANT: FAX NUMBER: (619) 453-6991
TITLE OF INVENTION: Protein Toxins Active
NUMBER OF SEQUENCES: 27
                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: YES ANTI-SENSE: NO
                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1174 amino acids
                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA50.Cl
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/597,607
FILING DATE: 15-OCT-90
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MEDIUM TYPE: Floppy disk
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                                                                     ORIGINAL SOURCE:
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IMMEDIATE SOURCE:
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                               ORGANISM: Bacillus thuringiensis STRAIN: aizawai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                            TOPOLOGY:
                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: si
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              INDIVIDUAL ISOLATE:
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                                                                                                                                                                                                                                                 (904)372-5800
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RESULT 9
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; CLONE: 81A2
PCT-US95-10310-2
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                                                                                                                                                       SEQ ID NO:4:
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                                   Query Match
Best Local Sim
Matches 111;
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Best Local
                                                                                                                                                                                 FILING DATE: 14-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 353,8
                                                                                                                                                                                                                                                                                                         ent No. 5164180

APPLICANT: Payne, Jewel; Sick,
TITLE OF INVENTION: BACILLUS:
                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374 IMPTLGINVVQGVGFIQPNNGEVLYRRGTVDSLDELPIDGENSLVGYSHRL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             373 I-----VLHKVGLVPPEKAEEMY--EGLHAHLEKVGIDGVK--IDVIHLLEMLCEDYG
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   336 YWGGLR--
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nes 111; Conser
                                                                                                                                                                       FILING DATE: 18-MAY-1989
                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                       LENGTH: 1174
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                                                      Similarity
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                                      Conservative
   -PQVPGLPE---
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                                    2.5%; Score 107; DB 6;
19.6%; Pred. No. 0.14;
Live 82; Mismatches 181
                                                                                                                                                                                                                                           US/07/451,389
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                                                                                                                                                                                                                                                                                                              THURINGIENSIS ISOLATES ACTIVE
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     --ARVIQPVLSPGLQMTMEDLA-----VDK 372
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                                                                      Length 1174;
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                                          192;
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RESULT 10
US-08-846-234-2
Sequence 2, Application US/08846234
Patent No. 6166292
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  INFORMATION FOR SEQ
                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,234
                                                           NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: OSUMI Chieko
APPLICANT: NOZAKI Jinshi
APPLICANT: KIDA Takao
                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: RAFFINOSE SYNTHASE GENE, METHOD FOR TITLE OF INVENTION: PRODUCING RAFFINOSE, AND TRANSGENIC PLANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      373
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                                                                                                                                                                                                                                                                                                                                                        AUDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     825 V-GCTDLQ-----EDLG 835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                642 PISIEGV--KTFALYLYQAKKLILSK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            596 IPVDATFEAEYDLERAQKAVNSLFTS---SNQIELKTDVTDYHIDQVSNLV---DCLSDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        555 LPDGSILRSEY---YALPTRDCLFEDPLHNGETMLKI----WNLNKFTGVIGAFNCQGGG 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                546 TMSANGSLTSQSFRFAEFPVGIST-----SGSQTAG-ISISNNPGRQTFHLDRIEF
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                                                                                                                                                                                                                                                                                                                     ZIP: 22202
                                     TELEPHONE:
                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VPGTGSLWPLSVE-SPIGRCGEPNR--CVPHLEWNPDLDCSCRDGEKCAHHSHHFSLDID 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YVTLPGTFDECYPTYLYQ--KIDESKLKAYNRYQLRGYIEDSQDLEIYLIRYNAKHETVN 767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSPVTKLIQTSLHFAPIGLVNMLNTSGAIQSVDYDDDLS-----SVEIG
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E: (703)-413-3000
(703)-413-2220
TD NO: 2:
                                                                                                                                                                                                                                                                                                                                         USA
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; TYPE: amino acid; TOPOLOGY: linear; MOLECULE TYPE: peptide; FRAGMENT TYPE: internal US-08-846-234-2
                                 В
                                                                                                                                                                                           ; TOPOLOGY: 11; MOLECULE TYPE: US-08-305-505-6
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                                                                                                                     Query Match
Best Local Similarity
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ZIP: 53202
ZIP: 53202
COMPUTER READABLE FORM:
MEDDIUM TYPE: Floppy disk
MEDDIUM TYPE: TEM PC compatible
TOMPUTER: IBM PC compatible
TOMPUTER: TEM PC-DOS/MS-DOS
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Best Local Similarity
                                                                                                                                                                                                                                                                                 TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 520 amino acids
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APPLICANT: Miziorko,
                                                                                                                                                                                                                                                                                                                                                                      NAME: Baker, Jean C.
REGISTION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 65
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/072,040
FILING DATE: 02 JUNE 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS: LENGTH: 19 amino acids
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
413 LEM--LCEDYGGRVDLAKAYYKAMTKSINKHF-----KGNGVIASMEHCNDFMFLGTEA 464
                                                                    378 VGLVPPE-----KAE-EMYEGLHAHLEKVGIDGVKID------VIHL 412
                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Milwaukee
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                                 17 VGIVALEIYFPSQYVDQAELEKYDGVDAGKYTIGLGQAKMGFCTDREDINSLCMTVVQNL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (414) 277-5709
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411 East Wisconsin Avenue
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                                                                                                         Conservative
                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                               single
                                                                                                    2.4%; Score 100; DB 1;
19.0%; Pred. No. 0.18;
htive 59; Mismatches 111
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SYNTHASE PREPARATION WITH IMPROVED
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                                                                                                        Mismatches 111; Indels 180;
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                                                                                                                                       Length 520;
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                                                                                                                         ; MOLECULE TYPE: protein US-08-717-515-8
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US-08-717-515-8
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                                                       Matches 116;
                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1276 amino aci
                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: THERMOSTABLE DNA : TITLE OF INVENTION: BACILLUS PALLIDUS
                                                                                                                                         TOPOLOGY: 1:00
                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          465 ISLGRVGDDFWCTDPSGDPNGTFWLQGCHMVHCANDSLWMGNFIHPDWDMFQSTHPCAAF 524
                         311 KAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLPEA--RVIQPVLSPGLQMIMEDL 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                569 PTRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCRETRRNQCFSQYSKRVTSK
                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Belon-
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 84 KAFQDKL----
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/717,515 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U:
ZIP: 07417
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                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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-YPFTWDAV--RYNGKLIAYPIAVEALSLIYNKDLLPNPPKTWEEI 133
                                                                 2.4%;
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                                                                   Pred.
                                                                    Score 100; DB 1; Pred. No. 0.87;
                                                       Mismatches 192;
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                                                                                Length 1276;
                                                       Indels 166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08525654A
                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
              FILING DATE: 28-JAN-
PRIOR APPLICATION DATA:
                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: TRANSGLUTAMINASE OF INVENTION: CRASSOSTREA GIGAS
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                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                APPLICATION NUMBER: FILING DATE: 28-SE
                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                      STREET: 1755 S. CITY: ARLINGTON
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 APPLICATION NUMBER:
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1755 S.
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                              28-JAN-1994
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    JP 7/3876
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478 DPSGDPNGTFWLQGCHMVHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAAS-----RAI
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Version #1.30
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; ORIGINAL SOURCE:
; ORGANISM: Crassostres
US-08-525-654A-1
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TELEPAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.3%; Score 98.5; DB 1; Length 770; Best Local Similarity 19.5%; Pred. No. 0.51; Matches 134; Conservative 72; Mismatches 241; Indels 239; Gaps
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ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                     695 IAVEG------SGLLAPQTID------ISSPIKPGDEVKKTVVLRPRKPYYWGRELIA 740
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741 TETSKQIVDIE----TSADIKVI 759
                                                                                                                                                                                  639 -SGKNIDSGSMESTQISFVLKKPQLVIQV---PQTIEAKEETEATIVFKNTTQLVLTQAE 694
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                                          755 KYDODOMYVVOVPWPIDSSSGGISVI 780
                                                                                                                                     697 FAPIGLVNMLNTSG--AIQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRACRIDGEDVGF 754
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QY 413 LEMLCEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDF	Db 261 DDPVLDVALQLLLEGGLSDVACTSPVS	QY 353 IQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVIHL	QY 304RAGQKGMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLPEARV : : : : : Db 208 ENESMIILFNAWAKEDTVYMDKEGERGEYVLNETGRVWTSRTWYG-RPWNFGQF	Qy 261 DSDPITK-EGMNQTVAGEQMPCRLLKFQENYKFRDYVNPKATGP	Query Match 2.3%; Score 98.5; DB 1; Length 771; Best Local Similarity 19.5%; Pred. No. 0.51; Matches 134; Conservative 72; Mismatches 241; Indels 239	SOURCE: M: Cra	; STRANDEDNESS: single ; TOPOLOGY: linear ; MOLECULE TYPE: protein	LENGTH: 771 amino TYPE: amino acid	; INFORMATION FOR SEQ ID NO: 3: ; SEQUENCE CHARACTERISTICS:	; TELEPHONE: 703-413-3000 ; TELEPAX: 703-413-2220	REGISTRATION NUM REFERENCE/DOCKET ETECOMMUNICATION	`	; APPLICATION NUMBER: JP 7/3876 ; FILING DATE: 13-JAN-1995	DATA:	; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: JP 6/8283	435	m 7	; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: PatentIn Release #1.0, Version #1.30	<pre>; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compatible</pre>	; ZIP: 22202 ; COMPUTER READABLE FORM:	; STATE: VA ; COUNTRY: USA	STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400	H H H	; TITLE OF INVENTION: CRASSOSTREA GIGAS ; NUMBER OF SEQUENCES: 150 . CORRESSONDENCE ADDRESS.	NVENTION: TRANSGLUTAMI	SEGURO,	WA,	36356 RMATION:	US-08-525-654A-3 ; Sequence 3, Application US/08525654A	
FMFLG 461	: vsvirc 291	SIDGVKIDVIHL 412	RPQVPGLPEARV 352 : RPWNFGQF 260	NPKATGP 303 	77																		TADT,							

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Patent No. 5668001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                 TELEFAX: (414) 277-5591 INFORMATION FOR SEQ ID NO:
                                                      REFERENCE/DOCKET NUMBER: 65
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5709
                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/072,040
FILING DATE: 02 JUNE 1993
                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                          NAME: Baker, Jean C.
REGISTRATION NUMBER: 35,433
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -SGKNIDSGSMESTQISFVLKKPQLVIQV---PQTIEAKEETEATIVFKNTTQLVLTQAE 695
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411 East Wisconsin
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3-HYDRAY-3-METHYLGLUTARYL-COA
SYNTHASE PREPARATION WITH IMPROVED
STABILITY
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; LENGTH: 520 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-305-505-4
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         378 VGLVPPE-----KAE-EMYEGLHAHLEKVGIDGVKID------VIHL 412
                                                          275 L--ARMFLNDFLN------DQNRDKNSIYSGLEAFGDVKL----
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                                                                                                                                                                                                                                                                                                                                                                                                                           17 VGIVALEIYFPSQYVDQAELEKYDGVDAGKYTIGLGQARMGFCTDREDINSLCLTVVQNL
DRDVEK 317
                            KYDQDQ 760
                                                                          LHFAPIGLVNMLNTSGAIQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRACRIDGEDVGF 754
                                                                                                                                              EWHSGENPISIEGVKTFALYLYQAKKLILSKPSQDLDIALDPFEFELITVSPVTKLIQTS
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                                                                                                                                                                                                                                                                      PCAAFHAASRAISGGPIYVSD-----SVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCL
                                                                                                                                                                                                                                                                                                                                  ISLGRYGDDFWCTDPSGDPNGTFWLQGCHMVHCANDSLWMGNF---IHPDWDMFQ--STH
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                                                                                                                   QW----
                                                                                                                                                                                                                                           PTGGVGAVALLIGPNAPLIFDRGLRGTHMQHAYDFYK----PD---MLSEY-----
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18.8%; Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63; Mismatches
                                                                                                                       ----QKEGNDNDFTLNDFGF-MISHSPYCKLVQKS
                                                                                                                                                                                 -CYLSALDRCYSVYRKKIRA-----
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Search completed: November 30, 2001, 09:43:45 Job time: 204 sec

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